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Date: Jun 6, 2002 2:32 PM  
About: Results were produced by the GenCore software, version 4.5.  
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Query length: 193  
Database: Issued\_Patents\_NA.\*  
Database sequences: 383533  
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; Sequence 1, Application US/08798897  
; Patent No. 5789201  
; GENERAL INFORMATION:  
; APPLICANT: Guatella, John  
; TITLE OF INVENTION: Genes Coding For Bcl-2  
; TITLE OF INVENTION: Homologue  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; ADDRESS: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/798,897  
; FILING DATE: February 11, 1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 1483.0140001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2500  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 579 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cDNA  
; US-08-798-897-1

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seq\_name: /cgn2\_6/prodata/1/ina/5B\_COMB.seq:us-08-978-523-1

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; Patent No. 5883228
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483, 0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; US-08-978-523-1

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alignment_scores:
Quality: 1002.00 Length: 193
Ratio: 5.192 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 98.964

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84 spgIleuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
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; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John

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TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2  
 TITLE OF INVENTION: Homologue  
 NUMBER OF SEQUENCES: 53  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 STREET: 1100 New York Avenue, N.W., Suite 600  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/798,897  
 FILING DATE: February 11, 1997  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Esmond, Robert W.  
 REGISTRATION NUMBER: 32,893  
 REFERENCE/DOCKET NUMBER: 1483.0140001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-2600  
 TELEFAX: 202-371-2540  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 579 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: both  
 MOLECULE TYPE: cDNA  
 US-08-798-897-2

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51 |||||
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seq\_documentation\_block:  
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 Patent No. 5883229

GENERAL INFORMATION:  
 Applicant: Guastella, John

TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2

TITLE OF INVENTION: Homologue

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 STREET: 1100 New York Avenue, N.W., Suite 600  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/978,523  
 FILING DATE: herewith

CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/798,897  
 FILING DATE: February 11, 1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:  
 NAME: Esmond, Robert W.  
 REGISTRATION NUMBER: 32,893  
 REFERENCE/DOCKET NUMBER: 1483.0140002

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-2600  
 TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 579 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: both  
 MOLECULE TYPE: cDNA  
 US-08-978-523-2

alignment\_scores:                   Length:   193  
                   Quality:   992.00           Gaps:   0  
                   Ratio:   5.167  
 Percent Similarity: 99.482   Percent Identity: 97.927

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151  TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
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Align seg 1/1 to: US-08-978-523-2 from: 1 to: 579

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17 eValAlaThrArgLeuArgGlnLysGlyThrValAlaGlyAlaGlyPro 34
1 TGTAGTTATAGCTGAGGCGAAGAGGTTATGCTGTGGAGCGGCCCGCG 100
34 LysGlnGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
101 GGGAGGCGCCAGCAGCTGACCCACCTGACCAACAGCCATGGGGCAGCTGA 150
51 AspLeuPheGlnThrArgPheArgThrPheSerAspLeuAlaAlaG1 67
151 GATGAGTTGAGACCCGCTCCGGCCACCTTCTCTGATCTGGCGCTCA 200
67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSera 84
201 GCTGCATGTCACCCAGGCTCAGCCCAACAGCTTCAACAGGCTCTCG 250
84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
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101 ValPheGlyAlaAlaLeuValAlaGlnSerValAsnLysGlnMetGlyPro 117
301 GCTTTGGGCTGCTGACCTGTGCTGAGTGTCAACAGAGGATGAGAAC 350
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351 ACTGTGGAGACAAGTCAGAGAGTGTGATGTGGCTTCTGAGAGCGGCG 400
134 eValAlaAspTrpIleHisSerSerGlyThrPheAlaGlnPheThrAlaLeu 150
401 TGGCTGATGATCCACAGCAGTGGGGCTGGGCGGAGTTCAACAGCTCA 450
151 TyrGlyAspGlyAlaLeuGlnGlnAlaArgArgLeuArgGlnGlyValSer 167
451 TACGGGGAGCGGGCGCCGAGAGAGCGCGGCTGTGGGAGGGAGAACTG 500
167 pAlaSerValArgThrValLeuThrGlnValAlaAlaLeuGlnAlaLeu 184
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Sequence 5, Application US/08081448  
 Patent No. 5646008  
 GENERAL INFORMATION:  
 APPLICANT: Thompson, Craig B.  
 APPLICANT: Boise, Lawrence H.  
 TITLE OF INVENTION: Vertebrate Apoptosis Gene:  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Arnold, White & Durkee  
 STREET: 321 No. 3646008th Clark Street, Suite 800  
 CITY: Chicago  
 STATE: IL  
 COUNTRY: USA  
 ZIP: 60610  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/081,448  
 FILING DATE: 19930622  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: No. 5646008thrup, Thomas E.  
 REGISTRATION NUMBER: 33,268  
 REFERENCE/DOCKET NUMBER: ARCD090  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312-744-0090  
 TELEFAX: 312-755-4489  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 926 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 135..836  
 US-08-081-448-5

## alignment\_scores:

Quality: 424.50 Length: 224  
 Ratio: 2.989 Gaps: 4  
 Percent Similarity: 63.393 Percent Identity: 40.179

## alignment\_block:

US-09-155-327E-9 x US-08-081-448-5

Align seg 1/1 to: US-08-081-448-5 from: 1 to: 926

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117 GlnValAlaGlnValAlaGlnAspTrpMetValAlaThrLeuGlnThrArg 134
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151 TyrGlyAspGlyAlaLeuGlnGlnAlaArgArgLeuArgGlnGlyValSer 167
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650 TTACCGAATGACCACTTGAACCTTGATCCAGAGAGAGCGGCTGGG 699
145 IacIuPheThrAlaLeuTyrgIyAspGlyAlaLeuGluGluAlaArgArg 161
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    ::::::::::::::::::::
750 GGCCAGAGAACGCTTCAACCGCTGGTCTCTGACGGCAGTACTGTGGCCG 799
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seq\_name: /c9n2\_6/ptodata/1/ina/5B\_COMB.seq:us-08-470-670A-6

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seq_documentation_block:
; Sequence 6, Application US/08470670A
; Patent No. 5834309
; Patent No. 5834309 5710045
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.
; TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470.670A
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,448
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARCD-090--1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135..836
; US-08-470-670A-6

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alignment\_scores:
Quality: 424.50
Ratio: 2.989

Length: 224
Gaps: 4

Percent Similarity: 63.393 Percent Identity: 40.179
Alignment\_block:
US-09-155-327e-9 x US-08-470-670A-6
Align seg 1/1 to: US-08-470-670A-6 from: 1 to: 926

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27 r.....
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28 .....ValGlyAlaGlyPro 33
250 AAGGAGCTGAATGAGAGATGAGACCCCAAGTGCATCAATGACCAACCA 299
34 .....GlyGluGlyProAlaAlaAsp.....40
300 TCCTGGACCTGGCAGACAGCCCGCGTGAATGAGACCACTGGCAGAC 349
41 .....ProLeuHisGlnA 45
350 CAGCAGTTTGGATGCCGAGAGTGATCCCATGACAGCAGTAAGACAG 399
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500 CTTTGAACAGTATGATGAATGAATCTTCCGAGATGGGATGAACCTGG 549
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    ::::::::::::::::::::
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112 AsnysglumetgluProleuValGlyGlnValGlnAspTrpMetValAl 128
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145 IacIuPheThrAlaLeuTyrgIyAspGlyAlaLeuGluGluAlaArgArg 161
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162 LeuArgGlu.....GlyAsnTrpAlaSerValArgThrValLeuThrGl 176
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176 yAlaValAlaLeuGlyAlaLeu 183
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seq\_name: /c9n2\_6/ptodata/1/ina/6A\_COMB.seq:us-08-481-739-1

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seq_documentation_block:
; Sequence 1, Application US/08481739
; Patent No. 6143291
; GENERAL INFORMATION:
; APPLICANT: June, Carl H. and Thompson, Craig B.
; TITLE OF INVENTION: METHODS FOR ENHANCING T CELL SURVIVAL
; TITLE OF INVENTION: BY AUGMENTING BCL-XL PROTEIN LEVELS
; NUMBER OF SEQUENCES: 4

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CORRESPONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,739
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,518
FILING DATE: 04-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Deconfil, Giulio A. (GAD)
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: RPI-034CP
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 135..836
US-08-481-739-1

alignment_scores:
Quality: 424.50 Length: 225
Ratio: 3.076 Gaps: 4
Percent Similarity: 61.333 Percent Identity: 40.889

alignment_block:
US-09-155-327e-9 x US-08-481-739-1 ..
Align seg 1/1 to: US-08-481-739-1 from: 1 to: 926

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27 T..... 27
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27 ..... 27
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35 uGlyProAlaAlaAsp.....ProLeuIleG 44
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seq_documentation_block:
Sequence 1, Application US/09167921A
Patent No. 6172216
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett P.
APPLICANT: Nickoloff, Brian J.
APPLICANT: Zhang, QingQing
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
FILE REFERENCE: ISPH-0324
CURRENT APPLICATION NUMBER: US/09/167,921A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 926
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (135)..(836)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: U20121 Genbank
DATABASE ENTRY DATE: 1994-07-26
US-09-167-921-1

alignment_scores:
Quality: 424.50 Length: 224
Ratio: 2.989 Gaps: 4
Percent Similarity: 63.393 Percent Identity: 40.179

alignment_block:
US-09-155-327e-9 x US-09-167-921-1 ..
Align seg 1/1 to: US-09-167-921-1 from: 1 to: 926

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162 LeuArgGlu.....GlyAsnTPRAlaSerValArgThrValLeuThrGl 176

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176 yAlaValAlaLeuGlyAlaLeu 183

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seq\_documentation\_block:

Sequence 39, Application US/09277020

Patent No. 6210892

GENERAL INFORMATION:

APPLICANT: Bennett, C. Frank

TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation

FILE REFERENCE: ISPH-0339

CURRENT FILING DATE: US/09/277,020

EARLIER FILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 39

LENGTH: 926

TYPE: DNA

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1  ORGANISM: Homo sapiens
US-09-277-020-39

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    Quality: 424.50      Length: 224
    Ratio: 2.989         Gaps: 4
    Percent Similarity: 63.393      Percent Identity: 40.179

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27  T..... 27
    |
200  CAGCTGAGTCACTTTAGTATGTGAAGAGAACAGACGACTGAGGCCAC 249
28  ..... 28
    |
250  AAGGACTGAATCGAGATGAGAACCCCAAGTGCATCAATGCAACACCA 299
34  .....GlyGlnGlyProAlaAlaAsp..... 40
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41  .....ProLeuHisGlnA 45
350  CAGCAGTTTGATGCCCGGAGAGTGCATCCCATGSCACAGTAAGAAGCA 399
45  IAmETArgAlaAlaGlyAspGlnPheGlnTyrArgPheArgTyrPhe 61
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95  rGLeuValAlaPhePheValPheGlyAlaAlaLeuCysAlaGlnSerVal 111
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650  TTACCTCGAATGACACCTTACAGCCTTGGAATCCAGAGAACGGCGGCTGG 699
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750  GGCACGAGAGCGCTTCAACCCGCTGCTTCACGCGGCACTGTGCGCG 799
176  yAlaValAlaLeuGlnGlyAlaLeu 183
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Sequence 1, Application US/09323743
Patent No. 621496
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett P.
APPLICANT: Nickoloff, Brian J.
APPLICANT: Zhang, Qingling
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
FILE REFERENCE: ISPH-0368
CURRENT APPLICATION NUMBER: US/09/323,743
CURRENT FILING DATE: 1999-06-01
EARLIER APPLICATION NUMBER: 09/277,020
EARLIER FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 09/167,921
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 926
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (135)..(836)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: L20121 Genbank
DATE: 1994-07-26
US-09-323-743-1

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alignment_scores:
Quality: 424.50      Length: 224
Ratio: 2.989         Gaps: 4
Percent Similarity: 63.393   Percent Identity: 40.179

alignment_block:
US-09-155-327e-9 x US-09-323-743-1 ..
Align seg 1/1 to: US-09-323-743-1 from: 1 to: 926

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200 CAGCTGGAGTCAGTTAGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAG 249
28 .....ValCysGlyAlaGlyPro 33
250 AAGGAGCTGAATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 299
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41 .....ProLeuHisGlnA 45
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45 lAmetArgAlaAlaGlnAspGlnPheGlnThrArgPheArgThrPhe 61
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112 AsnLysGluMetGluProLeuValGlyGlnValGlnAspTrpMetValAl 128
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145 lAgLpPheThrAlaLeuTyrGlyAspGlnValAlaLeuGlnGlnAlaArg 161
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162 LeuArgLys.....GlyAsnTrpAlaSerValArgThrValLeuThrG 176
750 GGCAGAGAACGCTCAACCGCTGCTTCTGATGAGGAGATGATGATGAG 799
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seq_documentation_block:
Sequence 6, Application US/08461511A
Patent No. 630331
GENERAL INFORMATION:
APPLICANT: Thompson, Craig B. B.
TITLE OF INVENTION: VERTICATE APOPTOSIS GENE COMPOSITIONS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESS: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,511A
FILING DATE: 05-Jun-1995
CLASSIFICATION: UNKNOWN
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARCD:179
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 135..836
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alignment_scores:
Quality: 424.50      Length: 224

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Ratio:	2.989	Gaps:	4
Percent Similarity:	63.393	Percent Identity:	40.179

Percent Similarity: 63.393

Percent Identity: 40.179

alignment\_block:

US-09-155-327E-9 x US-08-461-511A-6 . .

Align seg 1/1 to: US-08-461-511A-6 from: 1 to: 926

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CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: United States of America
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07089
FILING DATE: CONCURRENTLY FILED
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/081,448
FILING DATE: 22 JUNE 1993
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-320-7200
TELEFAX: 713-789-2679
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 135..836
PCT-US94-07089-6

alignment_scores:
Quality: 424..50 Length: 225
Ratio: 3.076 Gaps: 4
Percent Similarity: 61.333 Percent Identity: 40.889

alignment_block:
US-09-155-327E-9 x PCT-US94-07089-6 ..

Align seq 1/1 to: PCT-US94-07089-6 from: 1 to: 926

11 ArgAlaleuValAlaAspRphYeAljYtYrGArLeuAGlnLysGLyT 27
||| |||||||:|||||:|||||:||||| |||||||
150 CGGAGCTGGTGTTGACTTTCCTCCACAGCTTCCSACAAGAAGATA 199
27 T..... 27
200 CAGCTGCAGTCAGTTTAGTGTATGTAAGAAAGAAAGACTGAAGSSCA 249
27 ..... 27
250 AAGGACTGAATCGAGATGAGACCSCCAGTGCATCATGSCAASCCA 299
28 .....ValcysgylAlaglyProglycl 35
300 TCCTGGCACCTGCCAGACAGCCSCGGGTGATGAGACC...ACTGCCA 346
35 uGlyProAlalaaPr.....ProleuInsg 44
::: ::|||
347 CAGACGACGTTTGATGCCCGGAGAGGTATPSSCATGSCAGCATAAAC 396
44 InAlaMetArgAlaAlaGlYAspRgluPhesgluThArgrHeatgatgtthr 60
||||:|||| ||||||:||||| |||:||||:
397 AAGCGCTCAGGAGGACGAGCGAACGATTTGAACCTCGGATCCSGCGGSCA 446
61 PhesrAspLeuAlaAlaGlnLeuInHValThrProGlySerAlaGlnG 77

```

```

: INFORMATION FOR SFO ID NO: 20:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 717 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
:
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..717
: US-08-465-485A-20
:
: alignment_scores:
:   Quality: 406.50      Length: 235
:   Ratio: 2.904        Gaps: 5
:   Percent Similarity: 59.574   Percent Identity: 36.596
:
: alignment_block:
: US-09-155-327E-9 x US-08-465-485A-20   ..
:
: Align seg 1/1 to: US-08-465-485A-20 from: 1 to: 717
:
: 9 AspThrArgAlaLeuValAlaAspPheValGlyTyrArgLeuArgGlnly 25
:   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:
: 28 GACACACCGGGAGATGTGTATGATGAGACATCATATATAGCTGTGCAGAG 77
:   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
: 25 sGlyTyrValGlySglYAlaGly..... 32
:   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
: 78 GGGCTACAGATGGGATGCGGGAGATGTGGGCGCGCCGCCCGGGGCGG 127
:   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
: 33 .....ProGlyGlu..... 35
:   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
: 128 CCCCCCGCACGGGGCATCTTCTCCCTCCAGCCCGGGGACACCCCATCCA 177
:   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
: 35 ..... 35
:   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
: 178 GCCGCACTCCGCGACCGCGTCCGAGGACCTCGCGCTGCAGACCCCGC 227
:   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
: 36 .....GlyProAlaAlaAspPro.....L 42
:   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
: 228 TGCCCCGGGGCGCGCCGCGGGGCGCTGCGCTCAGCCCGGTGCACCTGTGG 277
:   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
: 42 euHISglnAlaMetArgAlaAlaGlyAspGluPheGlnThrProGlySerAl 58
:   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
: 278 TCCACCTGGCCCTCCGCGCAACCGCGGACGACACTCTCCCGCGGTACCGC 327
:   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
: 59 ArgThrPheSerAspLeuAlaAlaGlnLeuHisValThrProGlySerAl 75
:   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
: 328 GCGCACTTCCGCGGATGTCCAGCCACTCTCACCCTGCAGCCCTTCACCC 377
:   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
: 75 agInGlnArgPheThrGlnValSerAspGluLeuPheGlnGlyGlyPro 92
:   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
: 378 GCGGGGACGCTTTCGCCAGCGGTGGTGGAGGAGCTTTCAGGAGCGGGGTGA 427
:   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
: 92 snTrpGlyArgLeuValAlaAlaPhePheValDheGlyAlaAlaLeuGlySAla 108
:   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
: 428 ACTGGGGGAGAGATTGTGGCTTTCAGTTTCGCTGGGGGTGCATGTGTGTG 477
:   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
: 109 GluSerValAsnLysGluMetGluProLeuValGlyGlnValGlnAspTr 125
:   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
: 478 GAGAGCCTCAACCGGAGATGTGCGCCCTGTGGACACATTCGCCCTGTG 527
:   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
: 125 pmetValAlaTyrLeuGlnThrArgLeuAlaAspTrpIleHisSerSerg 142
:   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
: 528 GATGACTAGTACTGTAACCGGACCTGCACACTCTGGATTCAGGATTAAG 577
:   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
: 142 LysGlyTrrPalaGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGlnGlu 158
:   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
: 578 GAGCGCTGGGATGCGCTTGTGTGAACCTATACGC.....CCACAC 615
:   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
: 159 AlaArgTrrGluArgGlnGluGlnGlnAsnTrpAlaSerValArgThrValLeu 175
:   |||||:|||||:|||||:|||||:|||||:|||||:|||||:

```





## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/228,704  
FILING DATE: 18-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 994,941  
FILING DATE: 23-DEC-1992  
APPLICATION NUMBER: 663,010  
FILING DATE: 19-MAR-1991  
APPLICATION NUMBER: 883,687  
FILING DATE: 09-JUL-1986  
SEQ ID NO: 1  
LENGTH: 4825  
5459251-1

## alignment\_scores:

Quality: 406.50 Length: 235  
Ratio: 2.904 Gaps: 5  
Percent Similarity: 59.574 Percent Identity: 36.596

## alignment\_block:

US-09-155-327E-9 x 5459251-1 ..

Align seg 1/1 to: 5459251-1 from: 1 to: 4825

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9 AspThrArgAlaLeuValAlaAspPheValGlyTrpArgLeuArgGlnIly 25
|||||
1486 GACACACCGGAGATAGTGTAGTACATCATTAAGCTGCGCAGAG 1535
25 sGlyTrpValCysGlyAlaGly..... 32
|||||
1536 GGGGTACGAGTGGGTGGGAGATGTGGGCGCGCGCGCGGGGGCGG 1585
33 .....ProGlyGlu..... 35
1586 CCCCCGACGGGATCTTCTCTCCACGCCGGGACACGCCCATCA 1635
35 ..... 35
1636 GCCGATCCCGGACCGGTCGCCAGACCTCGCGCTGCAGACCCCGGC 1685
36 .....GlyProAlaAlaAspPro.....L 42
1686 TGCCCCCGGCGCCCGCGGGCTCGCTCAGCCGCGTCCACCTGTGG 1735
42 euHisGlnAlaMetArgAlaAlaGlyAspGluPheGluTrpArgPheArg 58
|||||
1736 TCCACCTGGCCCTCCGCCAAGCGCGGAGACTTCTCCGCGCTACCGC 1785
59 ArgThrPheSerAspLeuAlaAlaGlnLeuHisValThrProGlySerAl 75
|||||
1786 GCGGACTTCCCGGAGATGTCCAGCAGACCTGACCTGACGCCCTTCA 1835
75 agInGlnArgPheThrGlnValSerAspGluLeuPheGlnGlyPro 92
|||||
1836 CCGGGGACGCTTTGCGACGCTGGTGGAGAGCTTTGAGGGAGCGGGGTGA 1885
92 snTrpGlyArgLeuValAlaPhePheValPheGlyAlaAlaLeuCysAla 108
|||||
1886 ACTGGGGAGAGATTGTGGCTCTTGTAGTGGTGGGTGATGTGTG 1935
109 GluSerValAsnLysGluMetGluProLeuValGlyGlnValGlnAspTr 125
|||||
1936 GAGAGCGTCAACCGGAGATGTGCCCTGTGGACACATCGCCCTGTG 1985
125 pMetValAlaTrpLeuGluTrpArgLeuAlaAspTrpIleHisSerSerG 142
|||||
1986 GATGACTGATGACTGACACCGGACCTGCACACCTGATCCAGATACG 2035
142 IyGlyTrpAlaGluPheThrAlaLeuTrpGlyAspGlyAlaLeuGluGln 158
|||||
2036 GAGGCTGGGATGCTTTGTGAACCTGTACGCG.....CCCAAGC 2073
```

```
159 AlaArgArgLeuArgGluGlyAsnTrpAlaSerValArgThrValLeuTrh 175
|||||
2074 ATGGCGCCTCTGTGTTGATTCTCCTGGCTGCTCTGTAAGACTCTGTCAG 2123
175 rGlyAlaValAlaLeuGlyAlaLeuValThrValGlyAlaPhePheAla 192
|||||
2124 TTGGCCCTG...GTGGAGCTTGCATCACCCCTGGTGGCTATCTGAGCC 2170
192 erLys 193
|||||
2171 ACAAG 2175
```



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•  
•  
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•

•

[illegible]

**TITLE** Direct Submission  
**JOURNAL** Submitted (10-JUL-2000)  
**Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama**

kanagawa 230-0045, Japan (E-mail: genome-res@ssc.riken.go.jp  
URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)  
COMMENT  
Please visit our web site (<http://genome.gsc.riken.go.jp/>)

kanaagawa 230-0045, Japan [E-mail: genome-res@gs.c.riken.go.jp],  
URL: <http://genome.gsc.riken.go.jp/>, Tel.: 81-45-503-9222,  
Fax: 81-45-503-9216)  
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for  
further details.  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues. First strand cDNA was primed with a primer  
[5'-GAGGACGAGAAGATCCAAAGACTCTTTTGTGGTTTTTNN 3'], cDNA was  
prepared by using trehalose thermo-activated reverse transcriptase  
and subsequently enriched for full-length by cap-trapper. cDNA went  
through one round of normalization to Rot = 10.0 and subtraction to  
Rot = 100.0. Second strand cDNA was prepared with the primer  
GAGGACGAGATTCCGACTTAATTAATTAATTCGCCCCCCCCC 3'. cDNA was cleaved  
with BamHI and XhoI. Vector: a modified plasmidscript KS(+) after  
bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3'  
end: BamHI. Host: DH10B.

**FEATURES**  
**source**

BASE COUNT	ORIGIN
396	a
473	c
628	g
452	t

alignment_scores:	
Quality:	1006.00
Ratio:	5.212
Percent Similarity:	100.000
alignment_block:	
Length:	191
Gaps:	C
Percent Identity:	99.482

Align seg 1/1 to: AK015644 from: 1 to: 1949

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17 eValGIyTyrArgLeuArgGlnIysGlyTyrValCysGlyIynAaGlyProG 34  
182 TGTAGCTATTAAGCTGAGGCGCAAGAGGTTATGTCTGTGGACCTGGCCCTG 233  
34 IyGlnGlyProAlaIaaAspProLeuHISGlnAlaMetArgAlaIaaGly 50  
232 GGGAAAGGCCACCGCCGACCGCGCTGCCACCAAGCATATGGGGGCTGTGGA 281  
51 AspGlnPheGlnThrArgPheArgArgThrPheSerAspLeuAlaIaaGly 67

```

282 GACAGGTTTGAGACCCGTTTCCGCCCCACCTCTCTGACCTGGCCGCTCA 331
67 pLeuHh1sValThrProGlySerAlaGlnAlaArgPheThrGlnValSerA 84
332 GCTACACGTCACCCACAGGCTCAGCCACGACAGCAAGCTTCCACCCAGGTTCCG 381
84 spcLuleupheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
382 ACCGACTTTTCCAAAGGGGGCCCTAACTGGGGCCGCTTGGCAATTCTTT 431
101 ValPheGlyAlaAlaLeuGlyAlaLeuGlyAlaLeuGlyAlaLeuGlyAla 117
432 GTCTTTGGGGCTGCCCTGTGCTGACAGTCAACAAGAAATGAGACC 481
117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGlnThrArgL 134
482 TTTGGTGGGACAAAGTCAGAGATTGGATGGTGGCTTACTGAGACACGTC 531
134 euAlaAspTrpTrpLeuHisSerSerGlyGlyTyrPalaGlnPheThrAlaLeu 150
532 TGCTGTACTGGATCCACAGACAGTGGGGGCTGGGGGAGTTCAACAGCTCA 581
151 TyrGlyAspGlyAlaLeuGlnGlyAlaAlaArgArgLeuAspGlnGlyAsnTr 167
582 TAGCGGGACACGGGGCCCTGGAGAGAGCACGGCGTCTGGGGAGGGGAACTCG 631
167 palAserValaArgThrValLeuThrGlyAlaValaAlaLeuGlyAlaLeuY 184
632 GGCATCATAGTAGAGACAGTGTGACGGGGGCGCTGGGCACACTGGGGCCCTGG 681
184 alThrValGlyAlaPhePheAlaSerLys 193
682 TAACGTGATGGGCGCTTTTGTGTACGACAG 710
seq_name: gb_hlc:AK004680

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DEFINITION	3'UTR	5'UTR	LINEAR	HTC	19-JAN-2005
ACCESSION	MS	musculus	adult	male	lung
VERSION	library,	clone:1200009124	Bc12-11ke 2,	full	insert
KEYWORDS	AK004680				sequence.
SOURCE	HTC: CAP	trapper.			
ORGANISM	Mus	musculus	(strain:C57BL/6J)	adult	male
REFERENCE	clone:11b1	RIKEN	full-length	enriched	mouse
AUTHORS	clone:1200009124.				CDNA
TITLE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:				
JOURNAL	Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.				
MEDLINE	1 (sites)				
PUBMED	Carninci, P. and Hayashizaki, Y.				
REFERENCE	High-efficiency full-length CDNA cloning				
AUTHORS	Meth. Enzymol. 303, 19-44 (1999)				
TITLE	99279253				
JOURNAL	2 (sites)				
MEDLINE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,				
PUBMED	Itch, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
REFERENCE	Normalization and subtraction of cap-trapper-selected cDNAs to				
AUTHORS	prepare full-length CDNA libraries for rapid discovery of new genes				
TITLE	Genome Res. 10 (10), 1617-1630 (2000)				
JOURNAL	20499374				
MEDLINE	11042159				
PUBMED	3 (sites)				
REFERENCE	Shibata, K., Itch, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,				
AUTHORS	Konno, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itch, M.,				
TITLE	Sunil, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Kashiwagi, K.,				
JOURNAL	Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,				
MEDLINE	Fujikake, S., Inoue, K., Togawa, K., Iwawa, M., Onara, E., Watanabe, M.,				
PUBMED	Okazaki, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J.,				
REFERENCE	Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.				
AUTHORS	RIKEN	integrated	sequence	analysis	(RISA)
TITLE	sequencing pipeline with 384 multiplexed capillary sequencer				



## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 1030)  
NHL-MGC http://mgc.nci.nih.gov/  
TITLE  
JOURNAL  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cga@pds-remail.nih.gov  
Tissue Procurement: DCTD/DRP  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
Plate: LLCM800 row: p column: 04  
High quality sequence start: 5  
High quality sequence stop: 709.  
Location/Qualifiers  
1. 1030

## FEATURES

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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
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/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: Lung; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; CDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."  
BASE COUNT 190 a 284 c 386 g 170 t  
ORIGIN

## alignment\_scores:

Quality: 945.00 Length: 190  
Ratio: 5.027 Gaps: 1  
Percent Similarity: 98.947 Percent Identity: 95.789

## Alignment block:

US-09-155-327E-9 x BE793530 ..

Align seg 1/1 to: BE793530 from: 1 to: 1030

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17 eValGlyTyrArgLeuArgGlnGlyTyrValGlyAlaGlyProG 34
|||||
194 TGTAGGTTTAAAGCTGAGCGAGAAAGGTTATGTCGTGGAGCTGGCCG 243
34 TgtGlyGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
|||||
244 GGGAGGGCCAGCAGCTGACCTGACCAACCAAGCGGGAGAGCTGGA 293
51 AspGluPheGluThrArgPheArgGlyThrPheSerAspLeuAlaG 67
|||||
294 GATGAGTTTCAGACCCGCTTCGGCCACCTTCTGATCTGGCGGCTTA 343
67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSera 84
|||||
344 GCTGCAATGTAACCCAGCTCAGCCCAACAGCTTACACCCAGGTCTCCG 393
84 spGluLeuPheGlnGlyGlyProAsnTyrGlyArgLeuValAlaPhe 100
|||||
394 ATGAACCTTTTCAAGGGGGCCCAACTGGGGCCGCTTGACCTTCTTT 443

```

```

101 ValPheGlyAlaAlaLeuGlyAlaGluSerValAsnGlyMetGluP 117
|||||
444 GCTCTTGGGGCTGCACCTGTGCTCAGAGTGTCAACAAGAGAGTGAAC 493
117 oLeuValGlyGlnValGlnAspTyrMetValAlaTyrLeuGluThrArg 134
|||||
494 ACTGCTGGGACAAAGTCAGAGAGTGGATGTGCTTACTGAGACGGGGC 543
134 eValAspTyrPheHisSerSerGlyGlyTyrPalaGluPheThrAlaLeu 150
|||||
544 TGGCTGACTGATCCACACAGCTGGGGCTGGGGGAGTTTCACAGCTCTA 593
151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlnGly 167
594 TACGGGAGCGGGCCCTGGAGAGACCGCCGCTCTCGGGAGGAGGAGC 643
167 pAlaSerValArgPheValLeuThrGlyAlaValAlaLeuGlyAlaLeu 183
|||||
644 GCATCAGTGTAGACAGTGTGCTGACGGGGGCTGCGACTGGGGGCTTGG 693
184 ValThrValGlyAlaPhe 189
|||||
694 GTAACGTAGGGGCTT 711
seq_name: gb_est1:AL157542
seq_documentation_block:
LOCUS AL157542 804 bp mRNA linear EST 24-FEB-2000
DEFINITION DKFZP761D0816.t1 761 (synonym: hamy2) Homo sapiens CDNA clone
ACCESSION AL157542
VERSION AL157542.1 GI:7057943
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 804)
AUTHORS Ansoerg,W., Winkner,U., Mewes,W., Well,B. and Wiemann,S.
TITLE EST (Ansoerg,W., Winkner,U., Mewes,H.W., Well,B. and Wiemann,S.)
JOURNAL Unpublished (1999)
COMMENT Contact: Ansoerg W
MIPS
Am KlopferSpitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
Heidelberg/Germany) within the CDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone (DKFZP761D0816) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
source
1. 804
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZP761D0816"
/clone_lib="761 (synonym: hamy2)"
/tissue_type="amygdala"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI"
BASE COUNT 150 a 217 c 294 g 142 t 1 others
ORIGIN

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## alignment\_scores:

Quality: 943.00 Length: 193  
Ratio: 4.911 Gaps: 0  
Percent Similarity: 99.482 Percent Identity: 97.927



alignment block:  
US-09-155-327E-9 x AL157542 ..

Align seg 1/1 to: AL157542 from: 1 to: 804

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1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
134 ATGGCAGACCCAGCCCTCGGCCAGACAGCGGCTCTGAGAGCTGAGACTT 183
17 eValIGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
184 TGTAGGTATTAAGCTAGACAGAGGTTATGTCTGTGAGACTGAGCCCG 233
34 LysGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
234 GGGAGGGGCCAGCAGCTGACCCCTGACCAAGCCATGGCGGAGCTGGA 283
51 AspGluPheGlnThrArgPheArgThrPheSerAspLeuAlaAlaGly 67
284 GATGAGTTCAGAGACCCCTTCGGCGGACCTTCTGATCTGGCGGCTCA 333
67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
334 GCTCATGTGACCCAGCTGACGCCCAACAGCTTCAACCCAGCTCTCCG 383
84 spGluLeuPheGlnGlyLysGlyProAsnTrpGlyArgLeuValAlaPhe 100
384 ATGAACCTTTTCAAGGGGCCCAACTGGGGCCGCTTGTAGCCTTCTTT 433
101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGlyP 117
434 GCTTTGGGGCTGCACCTGTGTGCNAGAGTGTCAACAGAGATGGAAAC 483
117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGlnThrArg 134
484 ACTGGTGGACAAAGTGCAGAGAGTGTGTGCTTACCTGAGACGCGGC 533
134 euAlaAspTrpIleHisSerSerGlyGlyTyrPalaGluPheThrAlaLeu 150
534 TGGCTGACAGCAAGTGCAGAGTGTGGGGCTGGGGAGTTACAGCTCA 583
151 TyrGlyAspGlyAlaLeuGlnGlnAlaArgArgLeuArgGluGlyAsnTr 167
584 TACGGGGACGGGCCCTGGAGAGAGCGCGCTCTGGCGGAGGGGAAGT 632
167 PalaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeu 184
633 GGCATCAGTGAAGACAGTGTGACGGGGCGCTGGCACT. GGGGCCCTGG 681
184 alThrValGlyAlaPhePheAlaSerLys 193
682 TAACTGTAGGGCCCTTTTGTCTAGCAAG 710

```

seq\_name: gb\_est2:BI770566

seq\_documentation\_block:

LOCUS BI770566 697 bp mRNA linear EST 25-SEP-2001

DEFINITION 603060362F1 NIH\_MGC\_122 Homo sapiens cDNA clone IMAGE:5209862 5',

ACCESSION BI770566 mRNA sequence.

VERSION BI770566.1 GI:15762144

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

TITLE NIH-MGC http://mgc.nci.nih.gov/

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: rgs@nsl.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.llnl.gov  
Plate: L1A11526 row: k column: 15  
High quality sequence start: 21  
High quality sequence stop: 695.  
Location/Qualifiers

FEATURES  
source  
1. 697  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5209862"  
/clone\_id="NIH\_MGC\_122"  
/lab\_host="DH10B"  
/note="Organ: pooled lung and spleen; Vector: pCMV-Sport6;  
Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA source  
anonymous pool of 24 week female lungs, 16 week female  
spleen, and 20-22 week male spleens. Library is oligo-dT  
primed and directionally cloned (EcoRV site is destroyed  
upon cloning). Average insert size 1.4 kb, insert size  
range 1-3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 026. Note:  
this is a NIH\_MGC Library."

BASE COUNT 121 a 202 c 248 g 126 t  
ORIGIN

alignment\_scores:  
Quality: 880.00 Length: 187  
Ratio: 4.835 Gaps: 5  
Percent Similarity: 97.326 Percent Identity: 95.722

alignment block:  
US-09-155-327E-9 x BI770566 ..

Align seg 1/1 to: BI770566 from: 1 to: 697

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1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
145 ATGGCAGACCCAGCCCTCGGCCAGACAGCGGCTCTGAGAGCTGAGACTT 194
17 eValIGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
195 TGTAGGTATTAAGCTAGACAGAGGTTATGTCTGTGAGACTGAGCCCG 244
34 LysGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
245 GGGAGGGGCCAGCAGCTGACCCCTGACCAAGCCATGGCGGAGCTGGA 294
51 AspGluPheGlnThrArgPheArgThrPheSerAspLeuAlaAlaGly 67
295 GATGAGTTCAGAGACCCCTTCGGCGGACCTTCTGATCTGGCGGCTCA 344
67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
345 GCTCATGTGACCCAGCTGACGCCCAACAGCTTCAACCCAGCTCTCCG 394
84 spGluLeuPheGlnGlyLysGlyProAsnTrpGlyArgLeuValAlaPhe 100
395 ATGAACCTTTTCAAGGGGCCCAACTGGGGCCGCTTGTAGCCTTCTTT 444
101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGlyP 117
445 GCTTTGGGGCTGCACCTGTGTGCNAGAGTGTCAACAGAGATGGAAAC 494
117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGlnThrArg 133
495 CACTGTGGGACAAAGTGCAGAGAGTGTGCTGAGAGTGTGAGAGAGAG 544
133 gluAlaAspTrpIleHisSerSerGlyGlyTyrPalaGluPheThrAla 150

```



```

FEATURES
  source
    Location/Vdata/leu1
      1. .643
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone="IMAGE:5218294"
        /clone_11b="NIH_MGC_118"
        /tissue_type="leukocyte"
        /lab_host="DH10B"
        /lab_vector="pCMV-Sport6; Site_1: NotI; Site_2: EcoRV
        (destroyed); RNA source leukocytes from anonymous pool of
        non-activated adult donors. Library is oligo-dT primed
        and directionally cloned (EcoRV site is destroyed upon
        cloning). Average insert size 1.7 kb, insert size range
        1.2-3 kb. Library is normalized and enriched for
        full-length clones and was constructed by C. Gruber
        (Invitrogen). Research Genetics tracking code 027. Note

```

	seq_name:	gb_est2:Bf785386	
	seq_documentation_block:		
LOCUS	Bf785386	815 bp	MRNA linear EST 12-JAN-2001
DEFINITION	602111728F1 NC1_GCAP_Kid14 Mus musculus cDNA clone IMAGE:4239798		
VERSION	5', mRNA sequence.		
ACCESSION	Bf785386		
KEYWORDS	Bf785386.1 GI:12090422		
SOURCE	EST.		
ORGANISM	house mouse. Mus musculus Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 815)		
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D.		

Email: [cgabbs@rmail.nih.gov](mailto:cgabbs@rmail.nih.gov)  
Tissue Procurement: Jeffrey E. Green, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MCC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://Image.lnl.nih.gov>  
Plate: LMA9683 row: h column: 07  
High quality sequence start: 3  
High quality sequence stop: 650.  
Location/Qualifiers  
I..815

BASE COUNT	166 a	212 c	296 g	141 t
ORIGIN	technologies. NOTE: This is a NCI-CCAP Library.			

[illegible]

US-09-155-327E-9 x BF785386

Align seg 1/1 to: BF785386 from: 1 to: 815

[illegible]

158 GUAAGAAArgLeuAArgGluGlysnrTrpAlaSerValArgrThrValLe 174  
||||| |||||  
447 GAAGCACGGGT.CTCCGAGAGCGACGG.GCATCACTGAGGACACTGCT 494  
||||| |||||  
174 uPrGrGlValAlaLalAleuGlyAlaLeuValThrValGIyAlaPhePhea 191  
||||| |||||  
495 GACGGGGGCCGTGGCAGT.GGGGCCCTGGTAACAATGTTGGGGCCTTTTTCG 543  
||||| |||||  
191 IaSerIys 193  
:::~::~:  
544 TAGCACGT 551

seq_name:	gb_est2:BG296789			
seq_documentation block:				
LOCUS	BG296789	792 bp	mrna	linear
DEFINITION	602396527F1 NIH_MGC_94	Mus musculus	cDNA	clone IMAGE:4511215 5',
ACCESSION	RNA sequence.			
VERSION	BG296789			
KEYWORDS	GI:13063794			
SOURCE	EST.			
ORGANISM	house mouse.			
	Mus musculus			

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (pages 1 to 79)	Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus	NIH-MGC <a href="http://mgc.nhl.nih.gov/">http://mgc.nhl.nih.gov/</a>	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
Contact: Robert Strausberg	ph.D.			

EMAIL: cga005-1@earthlink.net  
 Tissue Procurement: The Cepro Laboratory  
 CNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.lnl.gov  
 Plate: LRAM10394 row: e column: 08  
 High quality sequence stop: 713.  
 Location/Accession:

FEATURES	SOURCE	Location/Qualifiers
		1. 792
		/organism="Mus musculus"
		/db_xref="taxon:10090"
		/clone="IMAGE:4511215"
		/clone_lib="NIH-MGC_94"
		/tissue_type="retina"
		/lab_host="DH10B (phage-resistant)"
		/note="Organ: eye; Vector: pCMV-SPORT6; Site.1: NotI; Site.2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies Note: this is a NIH-MGC library."
BASE COUNT		174 a 201 c 246 g 171 t
ORIGIN		

alignment_scores:	
Quality:	739.00
Ratio:	5.097
Percent Similarity:	99.315
alignment_block:	
Length:	146
Gaps:	0
Percent Identity:	98.630

05-09-155-32/E-9 x BG298789 ..  
Align seg 1/1 to: BG298789 from: 1 to: 792

1 MetAlaIthrProIaSerThrProIaosphargAlaIeuValAlaIaSpH 17  
99 ATGCGACCCGACACCTTCAACCCGACACCGGGCTCTAGTGGTCACTT 148  
17 eValG1YrYrArgLeuArgInLysG1YrYrValGysG1YrAlaG1YrProG 34



## ORGANISM

Homo sapiens

## REFERENCE

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
1 (bases 1 to 758)  
NIH-MGC <http://mgs.nci.nih.gov/>  
National Institutes of Health, Mammalian Gene Collection (MGC)

## AUTHORS

Unpublished (1999)

## COMMENT

Contact: Robert Strausberg, Ph.D.

Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

<http://image.llnl.gov>

Plate: LAM11477 row: a column: 01

High quality sequence stop: 753.

## FEATURES

## source

Location/Qualifiers

1..758

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_image="5190792"

/clone\_lib="NIH\_MGC\_116"

/lab\_host="DH10B"

/note="Organ: pooled colon, kidney, stomach; Vector: PCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA

source anonymous pool of 3 colons, age 26 yo male, 49 yo

female, 71 yo male colon, 46 yo male kidney, and pool of 2

stomachs, 62 yo male and 70 yo female. Library is

oligo-dT primed and directionally cloned (EcoRV site is

destroyed upon cloning). Average insert size 1.4 kb,

insert size range 1-3 kb. Library is normalized and

enriched for full-length clones and was constructed by C.

Gruber (Invitrogen). Research Genetics tracking code

023. Note: this is a NIH-MGC Library."

## BASE COUNT

140 a 216 c 228 g 174 t

## ORIGIN

## alignment\_scores:

Quality: 576.00

Ratio: 5.143

Percent Similarity: 100.000

Percent Identity: 97.321

Length: 112

Gaps: 0

Cuts: 0

Gaps: 0

Cuts: 0

Gaps: 0

Cuts: 0

Gaps: 0

Cuts: 0

Gaps: 0

Cuts: 0

Gaps: 0

Cuts: 0

Gaps: 0

Cuts: 0

Gaps: 0

Cuts: 0

Gaps: 0

Cuts: 0

Gaps: 0

Cuts: 0

Gaps: 0

Cuts: 0

Gaps: 0

Cuts: 0

101 ValPheGlyAlaAlaLeuGlyAlaSerValAsn 112  
439 GTCCTTGGGCTGCACGCTGTCTGTAAGAGTTTC 474  
seq\_name: gb\_est2:BM191403

## seq\_documentation\_block:

LOCUS BM191403

DEFINITION da16a10.y1 NICHD XGC L11 Xenopus laevis cDNA clone IMAGE:5129734

5' similar to SW:ARL\_XENLA 091827 APOPTOSIS REGULATOR R1; mRNA

sequence.

BM191403

ACCESSION BM191403.1 GI:17527366

VERSION EST.

KEYWORDS African clawed frog.

SOURCE Xenopus laevis

ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

Xenopodinae; Xenopus.

REFERENCE NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS 1 (bases 1 to 601)

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

JOURNAL Tumor Gene Index

COMMENT Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)

Tissue Procurement: Martha Redbert, Steven L. Klein, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: Xenopus clones from this library are available

through the I.M.A.G.E. Consortium/LLNL at: [image.llnl.gov](http://image.llnl.gov)

Seq primer: -40RP from G100

High quality sequence stop: 386.

## FEATURES

## source

Location/Qualifiers

1..601

/organism="Xenopus laevis"

/db\_xref="taxon:8355"

/clone\_image="5129754"

/clone\_lib="NICHD XGC L11"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: liver; Vector: PCMV-SPORT6; Site\_1: NotI;

Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.4 kb. Constructed by Life

Technologies. Note: This is a Xenopus Gene Collection (XGC

) Library."

## BASE COUNT

149 a 125 c 189 g 138 t

## ORIGIN

## alignment\_scores:

Quality: 572.50

Ratio: 4.119

Percent Similarity: 84.756

Percent Identity: 66.463

Length: 164

Gaps: 1

Cuts: 0

Gaps: 0

Cuts: 0

Gaps: 0

Cuts: 0

Gaps: 0

Cuts: 0

Gaps: 0

Cuts: 0

Gaps: 0

Cuts: 0

Gaps: 0

Cuts: 0

Gaps: 0

11 ArgAlaLeuValAlaAspPheValAlaGlyTyrArgLeuArgGlnGlyTyr 27  
119 CGGGCTTTGGTGAGGATTTTGGCGGTCAAGTTATGCAACGATGCT 168  
27 rValGlyAlaGlyProGlyGlyProAlaAlaAspProLeuHisG 44  
169 TGT.....CCAGACCTGCAGGACACACATCTGCTTTCATT 209  
44 lAlaMetArgAlaAlaGlyAspGluPheGluThrArgPheArgThr 60  
210 CAGCTTGGGTGCTGAGGAGATGATTTGAGAGGACGATTCAGACAA 259

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/abb_xref="taxon:10090"
/clone="IMAGE:1050567"
/clone_lib="parsted mouse myotubes MPRB5"
/clone_lib="parsted"
/gal_top="c2c12"
/gal_host="dm108"
/note="Vector: p7373D-Pac (pharmacia) with a modified
polylinker. Site_1: EcoRI. Site_2: NotI. 1st strand cDNA"

```

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seq_name: gb_est2:BF204905
seq_documentation_block:
LOCUS      601 bp      mRNA      EST 06-NOV-2000
DEFINITION 601866778F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4105836 5',
ACCESSION  BF204905
VERSION     BF204905
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 601)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished. (1999)
JOURNAL     Contact: Robert Strausberg, Ph.D.
COMMENT     Email: cgapbs-remail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

```





```

94 1yArgLeuValAlaPhePheValPheGlyAlaAlaLeuCysAlaGluSer 110
||||:|||||
362 GCGTATAGTTGCATTGTTGTTGGCCGACCTGTGTGAGAG 411
||||:|||||
111 ValAsnLysGluMetGluProLeuValGlyGlnValGlnAspTrpMetVal 127
|||||:|||||
412 TGTAAACAAGAGATGTCCCTCTTCTGCCACGAGATCAAGACTGGATGGT 461
|||||:|||||
127 1AlaTyrLeuGluThrArgLeuAlaAspTrpLleHisSerSerGlyGlyT 144
|:::|||||
462 GACATATCTGAGACAACTGAGAGCTGGATTCAACAATGAGGCT 511
|||||:|||||
144 rPalGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArg 160
|||:|||||
512 TGAATGGATTCTAACTATATGGGAGTGTGCCATGAAGACCCAGG 561
|||||:|||||
161 ArgLeuArgGluGlyAsnTrpAlaSerValArgThrValLeuThrGly 176
|||||:|||||
562 ACCCAACGTGAGGGAATTGGCATCATCTTGAGACTTGTCTAACTGA 609
|||||:|||||

```





```

|||||
1 ATGGCAGCCCAAGCTCAACCCACACACAGGCTCTAGTGGCTGACTT 50
17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlnValaGlyProG 34
51 TGTAGCTATTAGCTGAGCAGCAAGGTTATGCTGTGAGCTGGCCCTG 100
34 LylGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
101 GGAAGGCCCAAGCCGACCCGCTGACCAAGCCATGCGGGCTGTGGA 150
51 AspGluPheGluThrArgPheArgTyrPheSerAspLeuAlaAlaG 67
151 GACGAGTTTGAAGACCCCTTCCGCCGACCTTCTGACCTGGCCGCTCA 200
67 nLeuHisValThrProGlySerAlaGlnAlaArgPheThrGlnVala 84
201 GCTACAGCTGACCCAGGCTCAAGCCCAAGCAAGCTTCACCCAGGTTCCG 250
84 sPgluLeuPheGlnGlyLysProAsnTrpGlyArgLeuValAlaPhePhe 100
251 ACGAACTTTTCCAAAGGGGGCCCTTAACGCGGCGCTGTGGAATCTTT 300
101 ValPheGlyAlaAlaLeuGlyAlaGlnSerValAsnLysGlnMetGlu 117
301 GTCCTTGGGGCTGCCCTGTCTGTGAGAGTGTCAACAAGAAATGAGAGC 350
117 oLeuValGlyLysValGlnAspTrpMetValAlaTyrLeuGluThrArg 134
351 TTTGGTGGGACAAAGTGCAGATTGATGGTGGCTACCTGAGACACGCTC 400
134 euaAlaAspTrpIleHisSerSerGlyTyrPalaGluPheThrAlaLeu 150
401 TGGCTGACTGATCCACAGCAGTGGGGCTGGGCGGAGTTCACTCTTA 450
151 TyrGlyAspGlyAlaLeuGlnGlnAlaArgArgLeuArgGlnGlyAsn 167
451 TACGGGACCGGCGCTCGAGAGGACGCGCGCTGGCGGAGGAGACTG 500
167 palAspValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeu 184
501 GGCATCAGTGAAGACAGTCTGACGCGGGCGCTGGGCGGAGCTGGG 550
184 alThrValGlyAlaPhePheAlaSerLys 193
551 TAACTGTAGGGCGCTTTTGTCTAGCAAG 579
seq_name: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:AAV28333
seq_documentation_block:
ID AAV28333 standard; cDNA; 579 BP.
XX
AC AAV28333;
XX
DT 02-OCT-1998 (first entry)
XX
DE Rat bcl-y gene.
XX
KW ss: bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT CDS 1..579
FT /product= bcl-y
FT /tag= a
FT /note= "No stop codon given"
XX
PN US5789201-A.
XX
PD 04-AUG-1998.
XX
PF 11-FEB-1997; 97US-0798897.

```

```

XX
PR 23-FEB-1996; 96US-0012201.
PR 11-FEB-1997; 97US-0798897.
XX
PA (COCE-) COGENSYS INC.
XX
PI Guastella J;
XX
DR WPI: 1998-446079/38.
DR P-PDSB; AAW61391.
XX
PT Nucleic acids encoding B-cell lymphoma-y protein - useful for
PT producing recombinant protein for use in treating uncontrolled cell
PT growth e.g. cancers
XX
PS Claim 2; Column 13/14; 27pp; English.
XX
CC The mammalian bcl-y genes encode a protein that is a member of the bcl-2
CC family, components in the cell death pathway. The bcl-2 family
CC have both apoptotic activity and the apoptosis blocking activity. bcl-y
CC falls in the apoptosis activity category. The recombinant protein may
CC be used to prevent uncontrolled cell growth, either by its direct
CC administration to recombinant genetic constructs to increase its
CC expression in vivo. Also, antisense constructs can be used in disorders
CC where prevention of cell death is desired.
XX
SQ Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 other:

alignment_scores:
Quality: 1002.00 Length: 193
Ratio: 5.192 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 98.964

alignment_block:
US-09-155-327E-9 x AAV28333
Align seg 1/1 to: AAV28333 from: 1 to: 579

1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAsp 17
|||||
1 ATGGCAGCCCAAGCTCAACCCACACACAGGCTCTAGTGGCTGACTT 50
17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlnValaGlyProG 34
|||||
51 TGTAGCTATTAGCTGAGCAGCAAGGTTATGCTGTGAGCTGGCCCTG 100
34 LylGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
|||||
101 GGAAGGCCCAAGCCGACCCGCTGACCAAGCCATGCGGGCGAGTGA 150
51 AspGluPheGluThrArgPheArgTyrPheSerAspLeuAlaAlaG 67
|||||
151 GACGAGTTTGAAGACCCGCTTCCGCCGACCTTCTGACCTGGCCGCTCA 200
67 nLeuHisValThrProGlySerAlaGlnAlaArgPheThrGlnVala 84
|||||
201 GCTACAGCTGACCCAGGCTCAAGCCCAAGCAAGCTTCACCCAGGTTCCG 250
84 sPgluLeuPheGlnGlyLysProAsnTrpGlyArgLeuValAlaPhePhe 100
|||||
251 ACGAACTTTTCCAAAGGGGGCCCTTAACGCGGCGCTGTGGAATCTTT 300
101 ValPheGlyAlaAlaLeuGlyAlaGlnSerValAsnLysGlnMetGlu 117
|||||
301 GTCCTTGGGGCTGCCCTGTCTGTGAGAGTGTCAACAAGAAATGAGAGC 350
117 oLeuValGlyLysValGlnAspTrpMetValAlaTyrLeuGluThrArg 134
|||||
351 ATTGTTGGGACAAAGTGCAGATTGATGGTGGCTTCACTGAGACACCT 400
134 euaAlaAspTrpIleHisSerSerGlyTyrPalaGluPheThrAlaLeu 150
|||||

```



XX DE Human bcl-w gene.  
 XX XX Spermatoogenesis: bcl-3 gene; Bcl-2; human; fertility; infertility;  
 KW animal model; ss.  
 XX OS Homo sapiens.  
 XX PN MO9913710-A1.  
 XX PD 25-MAR-1999.  
 XX PE 16-SEP-1998; 98WO-A000764.  
 XX PR 16-SEP-1997; 97AU-0009228.  
 XX PA (HALT-) HALT INST MEDICAL RES WALTER & ELIZA.  
 XX PI Adams J, Cory S, Gibson L, Koentgen F, Print C;  
 XX DR WPI: 1999-243890/20.  
 XX DR P-PSDB; AA053530.  
 XX PT An animal model exhibiting reduced levels of a Bcl-w protein and/or  
 XX PT protein associated with Bcl-w  
 XX PS Claim 3; Page 32; 52pp; English.  
 CC The present sequence is the human bcl-w gene encoding Bcl-w protein  
 CC (see AA053530), a pro-survival member of the Bcl-2 family which is  
 CC widely expressed and which is essential for spermatogenesis. The  
 CC invention relates generally to a method of treatment and to an  
 CC animal model for the identification of molecules and genetic  
 CC sequences useful for inducing or reducing fertility of male  
 CC animals. Methods are provided for inducing or reducing fertility of male  
 CC animals. Methods are provided for the treatment of infertility, or  
 CC for reducing fertility, by modulating spermatogenesis. An animal  
 CC model carries a mutation is at least one allele of the human or  
 CC murine bcl-w gene or in a gene associated with bcl-w. Such animals  
 CC have disorganized seminiferous tubules and are substantially  
 CC infertile, but possess no other major abnormalities as determined  
 CC by histological examination. They can be used to screen for  
 CC therapeutic molecules including genetic sequences capable of  
 CC inducing, enhancing or otherwise facilitating spermatogenesis in  
 CC animals, or which can induce infertility.  
 XX SQ Sequence 581 BP; 104 A; 155 C; 210 G; 112 T; 0 other;

alignment\_scores:  
 Quality: 997.00 Length: 193  
 Ratio: 5.166 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 98.446

alignment\_block:

US-09-155-327e-9 x AA053530

Align seg 1/1 to: AA053530 from: 1 to: 581

1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAsp 17  
 1 ATGGGACCCCGACGCTCGGCCGACACAGGGCTTGTGGCAGACTT 50  
 17 eValGlyTyrArgLeuArgGlnGlyTyrValCysGlyAlaGlyProG 34  
 1 TGTAGGTTATTAAGCTGAGGACAGAGGCTATGTCTGTGAGCTGGCCCG 100  
 34 TgtGlyGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50  
 101 GCGAGGCGCCAGCAGCTGACCCGCTGACCAAGCATTGCGGAGCTGCA 150  
 51 AspGluPheGlnThrArgPheArgArgThrPheSerAspLeuAlaAla 67  
 151 GATGAGTTGAGACCGCTTCGCGGCGACCTTCTGATCTGCGGCTCA 200

67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSer 84  
 201 GCTGCTGTGACCCCGACGCTCAGCCCAACAGCTTCACCGAGCTCCG 250  
 84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100  
 251 ATGAACCTTTTCACAGCGGCGCCCAACTGGGCGCCCTTGTAGCTCTT 300  
 101 ValPheGlyAlaAlaLeuCysAlaGlnSerValAsnGlyGlnMetGlu 117  
 301 GTCTTGGGCTGCACGTGTGTGAGAGTGTCAACAGAGATGAGAAC 350  
 117 OLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGlnThrArg 134  
 351 ACTGGTGACAGTGCACAGCAGTGGGGCTGGGCGAGTTCAACAGCTCA 400  
 134 euAlaAspTrpIleHisSerSerGlyTyrTrpAlaGluPheThrAlaLeu 150  
 401 TGGCTGACTGGATCCACAGCAGTGGGGCTGGGCGAGTTCAACAGCTCA 450  
 151 TyrGlyAspGlyAlaLeuGlnGluAlaArgArgLeuArgGlyAsnTr 167  
 451 TACGGGACGGGGCGCCCTGAGAGAGCGCGGCTCTGCGGAGGGAACTG 500  
 167 PalSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeu 184  
 501 GGCATCAGTGAAGACAGTGTGACGGGGCGCTGGCAGCTGGGGCGCTTG 550  
 184 AlThrValGlyAlaPhePheAlaSerLys 193  
 551 TAACGTAGGGGCTTTTGTGCTAGCAAG 579  
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 ID AAV28334 standard; cDNA; 579 BP.  
 XX AAV28334;  
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 XX  
 XX 02-OCT-1998 (first entry)  
 DT  
 XX  
 XX Human bcl-y gene.  
 DE  
 XX  
 XX ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.  
 KW  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FT 1..579  
 FT /\*tag= a  
 FT /product= bcl-y  
 FT /note= "No stop codon given"  
 PN  
 XX US5789201-A.  
 XX  
 XX PD 04-AUG-1998.  
 XX  
 XX PE 11-FEB-1997; 97US-0798897.  
 XX  
 XX PR 23-FEB-1996; 96US-0012201.  
 XX PR 11-FEB-1997; 97US-0798897.  
 XX  
 XX PA (COCE-) COCENSYS INC.  
 XX  
 XX PI Guastella J;  
 XX  
 XX DR WPI: 1998-446079/38.  
 XX DR P-PSDB; AAW61392.  
 XX  
 XX Nucleic acids encoding B-cell lymphoma-Y protein - useful for  
 XX PT producing recombinant protein for use in treating uncontrolled cell  
 XX PT growth e.g. cancers



PS XX Claim 3; Column 15/16; 27bp; English.

CC The mammalian bcl-2 genes encode a protein that is a member of the bcl-2  
CC family, components in the cell death pathway. The bcl-2 family  
CC have both apoptotic activity and the apoptosis blocking activity. bcl-2  
CC falls in the apoptosis activity category. The recombinant protein may  
CC be used to prevent uncontrolled cell growth, either by its direct  
CC administration to recombinant genetic constructs to increase its  
CC expression in vivo. Also, antisense constructs can be used in disorders  
CC where prevention of cell death is desired.

CC Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;

alignment\_scores:  
Quality: 992.00 Length: 193  
Ratio: 5.167 Gaps: 0  
Percent Similarity: 99.482 Percent Identity: 97.927

alignment\_block:  
US-09-155-327E-9 x AAV28334 ..

Align seg 1/1 to: AAV28334 from: 1 to: 579

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17 eValGlyTyrArgLeuArgGlnGlyTyrValGlyGlyAlaGlyProG 34
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51 TGTAGGTATTAAGCTGAGCCAGAGAGGTTATGCTGTGGAGCTGGCCG 100
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34 lVgJuglYProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
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101 GGGAGGGCCAGCAGCTGACCCACTGCACCAAGCATGCGGAGCTGGA 150
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51 AspGluPheGluThrArgPheArgThrPheSerAspLeuAlaGly 67
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67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
|||||
201 GCTGATGTGACCCAGGCTCTACGCCCAACAGCTTACCAGGCTCCG 250
|||||
84 sPgluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
|||||
251 ATGAACTTTTCAAGGGGCGCCCAACTGGGCGCGCTTGTAGCCTTCTT 300
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101 ValPheGlyAlaAlaLeuGlyAlaGluSerValAsnLysGluMetGluPr 117
|||||
301 GCTCTGGGGCTGCACCTGTGCTAGAGTGTCAACAAAGAGAGTGAACC 350
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351 ACAGGCGGAGCAAGTGCAGAGTGTGAGTGTCTACTGAGAGACCGCGC 400
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151 TyrGlyAspGlyAlaLeuGluGlnAlaArgArgLeuArgGluGlyAsnTr 167
|||||
451 TAGCGGAGCGGGGCGCTGGAGAGCGCGGCTGTGCGGAGGGAAGACTG 500
|||||
167 palaserValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuY 184
|||||
501 GGCATCTAGTAGGAGCACTGCTGACGGGGCGGCTGGGCACTGGGGCCCTG 550
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551 TAACTGTAAGGGGCGCTTTTGTCTAGCAAG 579

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seq\_name: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1999.DAT:AA15946  
seq\_documentation\_block:  
ID AAX15946 standard; cDNA; 579 BP.

AC AAX15946:  
XX  
XX 20-MAY-1999 (first entry)  
XX  
XX cDNA encoding the human bcl-2 protein.

DE Rat bcl-2 protein; Rbcl-2; human bcl-2 protein; Hbcl-2; bcl-2 homologue;  
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;  
KW multiple sclerosis; myocardial infarction; vitally induced cell death;  
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
KW premature cell death; cell death stimulator; prolonged cell life span;  
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;  
KW parasite; ss.

OS Homo sapiens.

PN US5883229-A.

PD 16-MAR-1999.

PF 25-NOV-1997; 97US-0978523.

PR 23-FEB-1996; 96US-0012201.

PR 11-FEB-1997; 97US-0798897.

PR 25-NOV-1997; 97US-0978523.

PA (COCE-) COGENSYS INC.

PI Guastella J;

DR WPI; 1999-214150/18.

DR P-PDB; AAW97392.

PT Novel bcl-2 homologues of the rat and human bcl-2 protein - useful  
PT for modulating programmed cell death

XX Disclosure; Columns 15-16; 26pp; English.

PS The present sequence encodes human bcl-2 protein (Hbcl-2). The  
CC specification also describes rat bcl-2 protein (Rbcl-2). Rbcl-2 and  
CC Hbcl-2 are homologues of the bcl-2 protein thought to be involved in  
CC programmed cell death (apoptosis and necrosis). Rbcl-2 and Hbcl-2  
CC proteins may be used to treat conditions associated with a disruption of  
CC the cell death pathway. If they act as cell death inhibitors, they may be  
CC used in therapies to treat subjects suffering from: strokes, head trauma,  
CC Alzheimer's Disease, neural and muscular degenerative diseases  
CC (especially multiple sclerosis), myocardial infarction, vitally induced  
CC cell death, aging, spinal cord injuries and amyotrophic lateral  
CC sclerosis- conditions where cells under go premature cell death as a  
CC result of triggers which may or may not be apparent. They may also be  
CC used in this way to develop cell lines which remain viable in culture for  
CC an extended period. In contrast, if they act as cell death stimulators,  
CC Rbcl-2 and Hbcl-2 may be used to treat conditions associated with  
CC prolonged cell life span such as cancer (especially Kaposi's sarcoma and  
CC lung cancer) and auto/hyperimmune diseases. They may also be used to  
CC cause cell death in, and hence control, parasites.

Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;

alignment\_scores:  
Quality: 992.00 Length: 193  
Ratio: 5.167 Gaps: 0  
Percent Similarity: 99.482 Percent Identity: 97.927

alignment\_block:  
US-09-155-327E-9 x AAX15946 ..

Align seg 1/1 to: AAX15946 from: 1 to: 579

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17 eValaGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
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51 TGTAGGTATTAAGCTGAGGACAGAGGTTATGTCTGTGACTGTGCCCCG 100
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67 nLeuHisValThrProGlySerAlaGlnAlaArgPheThrGlnValSerA 84
  |||||||
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117 OlLeuValGlyAlaGlnAlaGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
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401 TGGCTGACTGATCCACAGCAGATGGGGGCTGGCGGAGTTTCACAGTCTTA 450
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seq\_documentation\_block:

ID AAT96577 standard; DNA; 583 BP.

AC AAT96577;

XX 22-APR-1998 (first entry)

XX Human bcl-2 DNA.

XX Bcl-2; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;

XX diagnosis; degenerative disease; ss.

XX Homo sapiens.

XX Key location/Qualifiers

XX CDS 1..582

XX FT /tag a

XX FT /product= bcl-2

XX PN WC9735971-A1.

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XX 02-OCT-1997.
XX 27-MAR-1997: 97WO-AU00199.
XX 27-MAR-1996: 96AU-0008965.
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX Adams JM, Cory S, Gibson LM, Holmgren SP.
XX WPI: 1997-489635/45.
XX P-PSDB: AAR36047.
XX Nucleic acid encoding apoptosis related gene bcl-2 - used to induce
XX or inhibit cell survival, e.g. for treatment of cancer and
XX degenerative diseases
XX Claim 3; Page 48; 86pp; English.
XX This sequence encodes a novel human gene, bcl-2, from the bcl-2 gene
XX family, extracted from an adult brain library. This gene promotes cell
XX survival, so its modulation is useful in treatment of cancer or
XX auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's
XX disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia,
XX human immunodeficiency virus infection or in cell transplants.
XX Up-regulation of the gene can also be used to modify cell lines cultured
XX in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas
XX and to increase survival of primary explants during genetic modification.
XX It can be used to produce recombinant Bcl-2 for therapy, diagnosis,
XX antibody production or screening of potential modulators.
XX
XX Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other;

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alignment\_scores:

Quality:	Length:
Ratio: 990.00	193
Percent Similarity: 100.000	Gaps: 0
Percent Identity: 97.409	

alignment\_block:

US-09-155-327E-9 x AAT96577 ..

Align seg 1/1 to: AAT96577 from: 1 to: 583

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51 TGTAGGTATTAAGCTGAGGACAGAGGTTATGTCTGTGACTGTGCCCCG 100
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  |||||||
84 sPGLuLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
  |||||||
251 ACGAACCTTTTTCAGAGGGGGCCCAAGCTGGGGCCCTTTGAGCCCTCTTT 300
  |||||||
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134 eUAlaAspTrpIleHisSerSerGlyGlyTTPAlaGluPheThrAlaLeu 150
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401 TGTGTACAGTGCATCCACAGACAGTGGGGCTGGGCGAGTTCACAGCTCTA 450
151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
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451 TACGGGGAGCGGGCCCTGGAGAGCGCGCTGTGCGGAGGGGAACTG 500
167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGluAlaLeuV 184
501 GGCATCAGTGAAGACAGTGTCTACAGGGGCCCTGGCACTGGGGCCCTGG 550
184 aThrValGlyAlaPhePheAlaSerLys 193
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551 TAACTGTAGGGGCTTTTGTCTAGCAAG 579

seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAx25134
seq_documentation_block:
ID AAX25134 standard; DNA; 583 BP.
XX
AC AAX25134;
XX
XX 05-JUL-1999 (first entry)
XX
XX Human bcl-w gene derivative.
DE
XX Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
KM animal model; ss.
XX
XX Homo sapiens.
OS
XX W0913710-A1.
PN
XX 25-MAR-1999.
PD
XX 16-SEP-1998; 98WC-AU00764.
XX
XX 16-SEP-1997; 97AU-0009228.
XX
XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PA
XX Adams J, Cory S, Gibson L, Koentgen F, Print C;
PI
XX WPI: 1999-243890/20.
DR
XX P-PSDB; AAY05532.
DR
XX
XX An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT protein associated with Bcl-w
XX
XX Disclosure; Page 36; 52pp; English.
XX
XX The present sequence is described as a derivative of the human
XX bcl-w gene (see AAX25132) and encodes Bcl-w protein (see AAY05532), a
XX pro-survival member of the Bcl-2 family which is widely expressed
XX and which is essential for spermatogenesis. The invention relates
XX generally to a method of treatment and to an animal model for the
XX identification of molecules and genetic sequences useful for
XX inducing or reducing fertility of male animals. Methods are
XX provided for the treatment of infertility, or for reducing
XX fertility, by modulating spermatogenesis. An animal model carries
XX a mutation is at least one allele of the human or murine bcl-w gene
XX or in a gene associated with bcl-w. Such animals have disorganised
XX seminiferous tubules and are substantially infertile, but possess no
XX other major abnormalities as determined by histological examination.
XX They can be used to screen for therapeutic molecules including
XX genetic sequences capable of inducing, enhancing or otherwise
XX facilitating spermatogenesis in animals, or which can induce
XX infertility.

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XX
SQ Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other;

alignment_scores:
Quality: 990.00 Length: 193
Ratio: 5.130 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 97.409

alignment_block:
US-09-155-327E-9 x AAX25134 ..

Align seg 1/1 to: AAX25134 from: 1 to: 583

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51 TGTAGGTATTAAGCTCAGGACAGAGGTTATGTCTGTGAGCTGGCCCG 100
34 LysGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
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|||||
151 GATGAGTTGCAGACCCGCTTCGGCGCCACTTCTGTGATCTGGCGCTCA 200
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201 GCTGCATGTGACCCCAAGCTCAGCCAGCCAGCAAGCCTTCACCAAGTCTCCG 250
84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
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101 ValPheGlyAlaAlaLeuGlyAlaGluSerValAsnLysGluMetGluPr 117
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117 OLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
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351 ACTGTGGGACAAAGTGCAGAGTGTGCTACTGTGAGACAGCGGCC 400
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151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
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451 TACGGGGAGCGGGCCCTGGAGAGCGCGCTGTGCGGAGGGGAACTG 500
167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGluAlaLeuV 184
501 GGCATCAGTGAAGACAGTGTCTACAGGGGCCCTGGCACTGGGGCCCTGG 550
184 aThrValGlyAlaPhePheAlaSerLys 193
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551 TAACTGTAGGGGCTTTTGTCTAGCAAG 579

seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:AAY96578
seq_documentation_block:
ID AAY96578 standard; DNA; 581 BP.
XX
AC AAY96578;
XX
XX 22-APR-1998 (first entry)
XX
XX Mouse bcl-w DNA.
XX

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KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;  
 KW diagnosis; degenerative disease; ss.  
 OS Mus sp.

Key	Location/Qualifiers
FT CDS	1..507
FT	/*tag= a
FT	/product= bcl-w
FT	/note= "g"

MO9735971-A1.

02-OCT-1997.

27-MAR-1997; 97MO-AU00199.

27-MAR-1996; 96AU-0008965.

(AMRA-) AMRAD OPERATIONS PTY LTD.

Adams JM, Cory S, Gibson LM, Holmgren SP;

WPI: 1997-489635/45.

P-PSDB: AAM36048.

Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and degenerative diseases

Claim 3; Page 50-51; 86pp: English.

This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene family. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis, antibody production or screening of potential modulators.

Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 other:

alignment\_scores:

Quality:	977.00	Length:	193
Ratio:	5.142	Gaps:	0
Percent Similarity:	98.446	Percent Identity:	96.373

alignment\_block:

US-09-155-327E-9 x AAT96578 ..

Align seq 1/1 to: AAT96578 from: 1 to: 581

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1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspH 17
1 ATGGCCGACCCGACGCTCAACCCGACGAGGCTGTAGTGGCTGACTT 50
17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
1 TGTAGGCTATAGGCTGAGGACAGAGGTTATGTCTGTGGAGCTGGGCTG 100
34 LysGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
101 GGGAAAGCCGACGCGCCGACGCGCTGACCAAGCCATGGGCGCTCTGGA 150
51 AspGluPheGlnThrArgPheArgArgThrPheSerAspLeuAlaAlaG 67
151 GACGAGTTTGAGACGCGCTTCCGCGGCAACCTCTCTGACCTGGCGCTCA 200

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67 nLeuHisValThrProGlySerAlaGlnAlaArgPheThrGlnValSera 84
201 GCTACACGTGACCCAGGCTCAGCCAGACGACGCTTACACCGAGTTTCG 250
84 spGluLeuPheGlnGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
251 ACGAACCTTTTCCAGAGGGGCGCTTAACCTGAGGCGCTTGTGGCAATTC 300
101 ValPheGlyAlaAlaLeuGlnAlaGlnSerValAsnLysGlnMetGluPr 117
301 GTCTTTGGGGCTGCGCTGTGCTGAGAGTGTCAACAAAGAAATGAGACC 350
117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGlnThrArg 134
351 TTTGGTGGGACAACTCCAGATTGGATGTGCTGACCTGAGACACAGTC 400
134 eAlaAspTrpIleHisSerSerGlyTyrPalaGluPheThrAlaLeu 150
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151 TyrGlyAspGlyAlaLeuGlnGluAlaArgArgLeuArgGlnGlyAsnTr 167
451 TACGGGAGACGGGCGCTGAGAGACGACGCGGCTGCGGAGGCAACTG 500
167 PalaSerValArgThrValLeuThrGlyAlaValAlaLeuGlnValLeu 184
501 GGCATGACTGAGCACAGTGTGACGGGGCGGTGACCTGGGGCGCTCG 550
184 aThrValGlyAlaPhePheAlaSerLys 193
551 TAACGTAGGGGCGCTTTTCTCTAGCAAG 579

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seq\_name: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:AAK25135

seq\_documentation\_block:

ID AAK25135 standard; DNA; 581 BP.

AAK25135;

05-JUL-1999 (first entry)

Mouse bcl-w gene derivative.

Spermatogenesis; bcl-3 gene; bcl-2; mouse; fertility; infertility;

animal model; ss.

Mus sp.

Key	Location/Qualifiers
FT CDS	1..507
FT	/*tag= a

MO9913710-A1.

25-MAR-1999.

16-SEP-1998; 98MO-AU00764.

16-SEP-1997; 97AU-0009228.

(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

Adams J, Cory S, Gibson L, Kentgen F, Print C;

WPI: 1999-243890/20.

P-PSDB: AAY05533.

An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w

Disclosure: Page 38; 52pp: English.

The present sequence is described as a derivative of the mouse



|||||  
1 ATGGCACCCACGCTCGGCCAGACAGCGCTCTGTCGGCAGATT 50  
17 eValIGlyTyrArgLeuArgGlnGlyGlyTyrValGlySglYalagIyProG 34  
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CC The present invention provides a number of nucleic acid  
CC genes which are modified by the methylation of cytosines. The sequences  
CC can be used in the diagnosis and treatment of immune system disorders,  
CC including eye diseases such as retinopathy, neovascular glaucoma and  
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid









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AUTHORS	1 (bases 1 to 582) Gibson,L., Holmgreen,S.P., Huang,D.C., Bernard,O., Copeland,N.G., Jenkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M. and Cory,S.			
NOTES	bcl-w: a novel member of the bcl-2 family, promotes cell survival			

REFERENCE AUTHORS	TITLE JOURNAL
2 (Pages 1 to 58.) Gibson, L., Holmgreen, S. P., Huang, D. C. S., Bernard, O., Adams, J. M. and Cory, S.	Direct Submission Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and Rita Hall Institute of Medical Research, PO Royal Melbourne

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Ross,A.J., Maymrite,K.G., Moss,J.E., Parlow,A.F., Russell,L.D. and
Macgregor,G.R.
Bcl-w is required for testis homeostasis
Unpublished
2 (bases 1 to 3476)
Ross,A.J. and Macgregor,G.R.
Direct Submission
Submitted (21-OCT-1997) Center for Molecular Medicine, Emory
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429 ACGAACCTTTCCAGAGGGGCGCTTAAGTGGGCGCTTGTGGCATTTCTT 478
101 ValPheGlyAlaAlaLeuGlySerValAsnGlyGluMetGluPr 117
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479 GTCTTTGGGGCTGCCCTGTGTCTGAGAGTGCACAAAGAAATGCAACC 528
117 oleuValIglGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
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529 TTTGGTGGGACCAAGTCAGAGATGTGATGTGCTACCTGAGACAGCTC 578
134 euAlaAspTrpIleHisSerSerGlyGlyTyrPalGluPheThrAlaLeu 150
|||||
579 TGGCTGACTGATCCACAGCAGTGGGGCTGGCGGAGTTCACAGCTCTA 628

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151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167  
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 629 TACGGGAGCGGGCCCTGAGAGGACGAGGCGCTGCGGAGGAGGAACTG 678  
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 167 palAserValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184  
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 679 GGCATCAGTAGAGACAGTCTGACGGGGCGCTGGCAGTGGGGCCCTGG 728  
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 184 alThrValGlyAlaPhePheAlaSerLys 193  
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 729 TAACTGAGGGCCCTTTTGTCTAGCAAG 757

seq\_name: gb\_pat:AR020779  
 seq\_documentation\_block: 579 bp DNA linear PAT 05-DEC-1998

LOCUS AR020779  
 DEFINITION Sequence 1 from patent US 5789201.  
 ACCESSION AR020779  
 VERSION AR020779.1 GI:3975394

KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.

REFERENCE  
 1 (bases 1 to 579)  
 AUTHORS Guastella, J.  
 TITLE Genes coding for bcl-1 and bcl-2 homologue  
 JOURNAL Patent: US 5789201-A 1 04-AUG-1998;  
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 source 1..579  
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BASE COUNT 111 a 157 c 198 g 113 t  
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alignment\_scores:  
 Quality: 1002.00 Length: 193  
 Ratio: 5.192 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 98.964

alignment\_block:  
 US-09-155-327E-9 x AR020779 ..

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 34 LysGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50  
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 51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaG 67  
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 151 GACGAGTTTGGAGACCCGCTTCCGGCGACCTTCTGTGACTGGCCGCTCA 200  
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 67 pLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84  
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 251 ACGAACTTTTCCAGGGGGCCCAACTGAGGCGCTTGTGGCACTCTTT 300  
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 101 ValPheGlyAlaAlaLeuCysAlaGlnSerValAsnLysGluMetGluTr 117  
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117 OlauValGlyGlnValAlaAspTrpMetValAlaTyrLeuGluThrArgL 134  
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 184 alThrValGlyAlaPhePheAlaSerLys 193  
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 551 TAACTGAGGGCCCTTTTGTCTAGCAAG 579

seq\_name: gb\_ro:AF096291

seq\_documentation\_block: 582 bp mRNA linear ROD 28-FEB-2000

LOCUS AF096291  
 DEFINITION Rattus norvegicus Bcl-w (bcl-w) mRNA, complete cds.  
 ACCESSION AF096291  
 VERSION AF096291.1 GI:3747129

KEYWORDS  
 SOURCE Norway rat.  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE  
 1 (bases 1 to 582)  
 AUTHORS Hamer, S., Skoglosa, Y. and Lindholm, D.  
 TITLE Differential expression of bcl-w and bcl-x messenger RNA in the  
 developing and adult rat nervous system  
 JOURNAL Neuroscience 91 (2), 673-684 (1999)  
 MEDLINE 99292146  
 PUBMED 10366024

REFERENCE  
 2 (bases 1 to 582)  
 AUTHORS Hamer, S., Skoglosa, Y. and Lindholm, D.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-OCT-1998) Developmental Neuroscience, Uppsala  
 University, Box 587, BMC, Uppsala 751 23, Sweden  
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 /tissue\_type="brain"  
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 /product="Bcl-w"  
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 /db\_xref="GI:3747130"  
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 ARAAGDEFFRRFRFTDLAOLHLPFGSAQOFRFTQVSDLEFGGNNWRLVAFTYF  
 GAIDAESYKRNKMEPIVNGOVDMVYLETFLADMIHSSGMAEFTALYDGLAEAR  
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BASE COUNT 111 a 157 c 200 g 114 t  
 ORIGIN

alignment\_scores:  
 Quality: 1002.00 Length: 193  
 Ratio: 5.192 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 98.964

## alignment\_block:

US-09-155-327e-9 x AF096291

Align seg 1/1 to: AF096291 from: 1 to: 582

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17 eValGlyTyrArgLeuArgGlnLysGlyTyrValLysGlyAlaGlyProG 34
51 TGTAGGCTATATAGCTGAGCGAGAGAGGTTATGTCTGTGAGCTGGCCCTG 100
34 LysGlyGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
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51 AspGluPheGluThrArgPheArgThrPheSerAspLeuAlaAlaGly 67
151 GAGGAGTTTGAAGCCCGCTTCCGCGACCTCTCTGACCTGGCCGCTCA 200
67 nLeuHisValThrProGlySerAlaGlnAlaArgPheThrGlnValSerA 84
201 GCTACACGTGACCCAGGCTCAGCCAGCAGCAGCTTCAACCCAGCTTCCG 250
84 spGluLeuPheGlnGlyLysProAsnTrpGlyArgLeuValAlaPhePhe 100
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101 ValPheGlyAlaAlaLeuGlnCysAlaGlnSerValAsnLysGluMetGluPr 117
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117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
351 ATTGGTGGACAAAGTGCAGAGTGTGATGTGACCTGAGACAGACGCT 400
134 euAlaAspTrpIleHisSerSerGlyTyrAlaGluPheThrAlaLeu 150
401 TGGCGACTGTGATCCACAGCAGTGGGGCTGGGGGAGTTCCAGCGCTCA 450
151 TyrGlyAspGlyAlaLeuGlnGluAlaArgArgLeuArgGluGlyAsnTr 167
451 TACGGGAGCGGGGCGCTGGAGGAGCAGCGGCTGTGGCGGAGGGAACCTG 500
167 PalAspValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
501 GGCATCAGTGAAGACAGTGTGAGCGGGCGCTGTGGCAGCTGGGGCCCTGG 550
184 aThrValGlyAlaPhePheAlaSerLys 193
551 TAACTGTAGGGGCGCTTTTGTGTCAGCAG 579

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seq\_name: gb-pr:HSU59747

seq\_documentation\_block:

LOCUS HSU59747 582 bp mRNA linear PRI 29-SEP-1996

DEFINITION Human Bcl-2 (bcl-2) mRNA, complete cds.

ACCESSION U59747

VERSION U59747.1 GI:1572492

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 582)

AUTHORS Gibson, L., Holmgren, S.P., Huang, D.C., Bernard, O., Copeland, N.G., Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S.

TITLE bcl-2, a novel member of the bcl-2 family, promotes cell survival

JOURNAL Oncogene 13 (4), 665-675 (1996)

MEMLINE 96358615

REFERENCE 2 (bases 1 to 582)

## AUTHORS

Gibson, L., Holmgren, S.P., Huang, D.C., Bernard, O., Adams, J.M. and

## TITLE

Direct Submission

## JOURNAL

Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and

## FEATURES

Eliza Hall Institute of Medical Research, PO Royal Melbourne

## source

Hospital, Parkville, Victoria 3050, Australia

## gene

Location/Qualifiers

## CDS

1..582

## BASE COUNT

104 a 156 c 211 g 111 t

## ORIGIN

## alignment\_scores:

Quality: 997.00 Length: 193

Ratio: 5.166 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 98.446

## alignment\_block:

US-09-155-327e-9 x HSU59747

Align seg 1/1 to: HSU59747 from: 1 to: 582

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51 TGTAGGCTATATAGCTGAGCGAGAGGTTATGTCTGTGAGCTGGCCCTG 100
34 LysGlyGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
101 GGGAGAGGCCAGCAGCCGACCCCTGACCAACCATGGGGGAGCTGGA 150
51 AspGluPheGluThrArgPheArgThrPheSerAspLeuAlaAlaGly 67
151 GAGGAGTTTGAAGCCCGCTTCCGCGACCTCTCTGACCTGGCCGCTCA 200
67 nLeuHisValThrProGlySerAlaGlnAlaArgPheThrGlnValSerA 84
201 GCTACACGTGACCCAGGCTCAGCCAGCAGCAGCTTCAACCCAGCTTCCG 250
84 spGluLeuPheGlnGlyLysProAsnTrpGlyArgLeuValAlaPhePhe 100
251 ACGAATTTTCCAGAGGGGCGCCCACTGGGGCGCTTGTGTGGCATCTTT 300
101 ValPheGlyAlaAlaLeuGlnCysAlaGlnSerValAsnLysGluMetGluPr 117
301 GCTCTTGGGGCTGCGCTGTCTGTGAGTGTCAACAAGAAATGAGACC 350
117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
351 ATTGGTGGACAAAGTGCAGAGTGTGATGTGACCTGAGACAGACGCT 400
134 euAlaAspTrpIleHisSerSerGlyTyrAlaGluPheThrAlaLeu 150

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## KEYWORDS

SOURCE Homo sapiens male brain myoblast cell\_line:KG-1 cDNA to mRNA,  
clone.lib:psport 1 clone:HA6752.

## ORGANISM

Homo sapiens

## REFERENCE

1 (bases 1 to 3542)  
Mammalia; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euteleostomi; Primates; Catarrhini; Homidae; Homo.

## AUTHORS

## TITLE

## JOURNAL

DNA Res. 3 (5), 321-329 (1996)

## MEDLINE

97191544

## AUTHORS

Ohara, O., Nagase, T., Kikuno, R. and Nomura, N.

## JOURNAL

Submitted (27-AUG-1996) Osamu Ohara, Kazusa DNA Research Institute;  
1532-3, Yama, Kiserazu, Chiba 292-0812, Japan  
(E-mail:cdna@kazuza.or.jp, Tel:+81-438-52-3913)

## FEATURES

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1. 3542  
Location/Qualifiers

## ORGANISM

/organism="Homo sapiens"

## DB XREF

/db\_xref="taxon:9606"

## CLONE

/clone="HA6752"

## SEX

/sex="male"

## CELL LINE

/cell\_line="KG-1"

## CELL TYPE

/cell\_type="myoblast"

## TISSUE

/tissue="brain"

## CLONE LIB

/clone\_lib="psport 1"

## GENE

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## CDS

177..758  
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## BASE COUNT

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## ORIGIN

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(A24428)"

## CODON START

/codon\_start=1

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/protein\_id="BA19666.1"

## DB XREF

/db\_xref="GI:194418"

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AMRAAGDEFERFRFTSDLAOLHTVPGSAQORPTQVSDLEFGCGPNNGRVAVAFV  
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## ALIGNMENT SCORES

Quality: 997.00 Length: 193  
Ratio: 5.166 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 98.446

## ALIGNMENT BLOCK

US-09-155-327E-9 x D87461 ..

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to: D87461 from: 1 to: 3542

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|||||
277 GGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 326
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51 AspGluPheGluThrArgPheArgTyrThrPheSerAspLeuAlaGly 67
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## seq\_name: gb\_pat:AR020780

## seq\_documentation\_block:

LOCUS AR020780 579 bp DNA linear PAT 05-DEC-1998

DEFINITION Sequence 2 from patent US 5789201.

ACCESSION AR020780

VERSION AR020780.1 GI:3975395

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

BASE COUNT

ORIGIN

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67 nleuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSera 84
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117 OleuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
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134 euaAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
|||||
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151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
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451 TACGGGAGCGGGCCCTGGAGAGCGCGGCTGCGGGAGGGGAACGTG 500
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501 GGCATCAGTGAAGACAGTCTGACGGGGGCCGTGACCTGGGGCCCTGG 550
184 alThrValGlyAlaPhePheAlaSerLys 193
551 TAACTGTAGGGGCTTTTGTCTAGCAAG 579

seq_name: gb_pat:AX022529
seq_documentation_block: 583 bp DNA linear PAT 07-SEP-2000
LOCUS AX022529
DEFINITION Sequence 6 from Patent EP0932674.
ACCESSION AX022529
VERSION AX022529.1 GI:10046125
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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BASE COUNT 105 a 157 c 210 g 111 t
ORIGIN

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alignment_scores:
  quality: 990.00 Length: 193
  ratio: 5.130 Gaps: 0
  Percent Similarity: 100.000 Percent Identity: 97.409
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|||||
51 TGTAGTWTATAGCTGAGGAGAAAGGTTATGCTGTGTGAGCTGGGCGCG 100
34 LysGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
|||||
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|||||
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67 nleuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSera 84
|||||
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84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
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101 ValPheGlyAlaAlaLeuGlyAlaGlySerValAlaGlnGlyMetGluPr 117
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|||||
501 GGCATCAGTGAAGACAGTCTGACGGGGGCCGTGACCTGGGGCCCTGG 550
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seq_name: gb_pat:AX030817
seq_documentation_block: 583 bp DNA linear PAT 20-SEP-2000
LOCUS AX030817
DEFINITION Sequence 6 from Patent WO9735971.
ACCESSION AX030817
VERSION AX030817.1 GI:10278311
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
A novel mammalian gene, bcl-2, belongs to the bcl-2 family of
apoptosis-controlling genes

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## JOURNAL

Patent: WO 9735971-A 6 02-OCT-1997;  
ADAMS JERRY MCKEE (AU) ; HOLMGREN SHAUN P (AU) ; CORY SUZANNE (AU)

## FEATURES

; GIBSON LEONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)  
Location/Qualifiers

## source

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## CDS

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17 eValGlyTyrArgLeuArgGlnGlyTyrValCysGlyAlaGlyPro 34  
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101 GGGAGGGCCGACGCTGACCCGCTGCACCAACGCTGCGGACCTTGA 150  
51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaG 67  
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67 nLeuHISValThrProGlySerAlaGlnAlaArgPheThrGlnValSer 84  
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301 CTCTTTGGGGCTGCACTGTGCTGAGAGTGTCAACAAGAGATGGAC 350  
117 OleuValGlyValGlnAspTrpMetValAlaTyrLeuGlnThrArg 134  
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Ratio: 5.130 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 97.409

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US-09-155-327E-9 x AX030817

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184 alThrValGlyAlaPhePheAlaSerLys 193  
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seq\_documentation\_block:

LOCUS AX022531 581 bp DNA linear PAT 07-SEP-2000

DEFINITION Sequence 8 from Patent EP0932674.

ACCESSION AX022531

VERSION

KEYWORDS AX022531.1 GI:10046127

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 581)  
Adams,J.M., Holmgren,S.P., Cory,S. and Gibson,L.M.  
A novel mammalian gene, bcl-2, belongs to the bcl-2 family of  
apoptosis-controlling genes  
Patent: EP 0932674-A 8 04-AUG-1999;  
AMRAD OPERATIONS PTY LTD (AU)

FEATURES  
Location/Qualifiers

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/codon\_start=1  
/protein\_id="CAC07881.1"  
/db\_xref="GI:10046128"

1 ATGGCGACCCAGCCTCAACCCGACACAGCGGCTTATGCTGACTT 50  
17 eValGlyTyrArgLeuArgGlnGlyTyrValCysGlyAlaGlyPro 34  
51 TGTAGGTTATAGCTGAGGACAGAAAGGTTATGTTGTGAGCTGGCCCG 100  
34 1yGlnGlyProAlaAlaAspProLeuHISGlnAlaMetArgAlaAlaGly 50  
101 GGGAGGGCCGACGCTGACCCGCTGCACCAACGCTTCAACGCTTCCG 150  
51 AspGluPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 67  
151 GATGAGCTTGAAGACCCGCTTCCGGGCACTTCTGTGATCGGGGCTCA 200  
67 nLeuHISValThrProGlySerAlaGlnAlaArgPheThrGlnValSer 84  
201 GCTGCATGACCCAGGCTGACCCGCTTCAACGCTTCAACGCTTCCG 250  
84 sPGLuLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100  
251 ACGAACCTTTTCAAGGGGCCCCCAACTGGGGCCGCTTGTGACCTTTT 300

## alignment\_scores:

Quality: 977.00 Length: 193  
Ratio: 5.142 Gaps: 0  
Percent Similarity: 98.446 Percent Identity: 96.373

## alignment\_block:

US-09-155-327E-9 x AX022531

Align seg 1/1 to: AX022531 from: 1 to: 581

101 ValPheGlyAlaIalLeuGlyAlaGluSerValAsnLysGluMetGluPr 117  
 |||||  
 301 GTCTTGGGGCTGCCCTGTGCTGCTGAGAGTGTCAACAAGAAATGGAGCC 350  
 117 OleuValGlyGlnValGlnAspTTPMetValAlaTyrLeuGluThrArgL 134  
 |||||  
 351 TTTGGTGGGACAGTCCAGATGTGATCGTGGCTTACCTGTGAGACAGTTC 400  
 134 euaAlaAspTTPLeuHisSerSerGlyTTPAlaGluPheThrAlaLeu 150  
 |||||  
 401 TGGCTGACTGATCCACAGACAGTGGCGGCGGCGGACTTCACAGCTCTA 450  
 151 TyrGlyAspGlyAlaLeuGluGlnAlaArgArgLeuArgGluGlyAsnTr 167  
 |||||  
 451 TACGGGAGCGGGGCGCTGGAGAGCACGCGCTCGCGGAGGAGCAACTG 500  
 167 palAserValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeu 184  
 |||||  
 501 GGCATGATGAGACACAGTGTGACGGGGCGCTGGGCGGCGCTGG 550  
 184 alThrValGlyAlaPhePheAlaSerLys 193  
 |||||  
 551 TAACTTAGGGGCTTTTGTGCTAGCAAG 579

seq\_name: gb\_pat:AX030819

seq\_documentation\_block:

LOCUS AX030819 581 bp DNA linear PAT 20-SEP-2000  
 DEFINITION Sequence 8 from Patent WO9735971.  
 ACCESSION AX030819  
 VERSION AX030819.1 GI:10278313

KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS  
 TITLE

JOURNAL  
 1 (bases 1 to 581)  
 Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.  
 A novel mammalian gene, bcl-2, belongs to the bcl-2 family of  
 apoptosis-controlling genes  
 Patent: WO 9735971-A 8 02-OCT-1997;  
 ADAMS JERRY MCKEE (AU) ; HOLMGREEN SHAUN P (AU) ; CORY SUZANNE (AU)  
 ; GIBSON LEONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)  
 location/Qualifiers

FEATURES  
 source  
 1..581  
 /organism="unidentified"  
 /db\_xref="taxon:32644"

CDS

/note="unnamed protein product"  
 /codon\_start=1  
 /protein\_id="CAC09622.1"  
 /db\_xref="GI:10278313"  
 /translation="MPTPASTPDPTRALVADPVGVRRLRQKGVCGAGGEPADPLHQ  
 AMRAAGDEFERFRFTSDLAQLHVTGSAQOQFTQVSDRLPGGPNMGRIVAFVF  
 GAALCAESYKEMEPPLVSGQVQDWIVAYLETRLDWMHSSGGADFTALYGDGALEDKR  
 RLREGNMA"

BASE COUNT 105 a 164 c 195 g 117 t  
 ORIGIN

alignment\_scores:  
 Quality: 977.00 Length: 193  
 Ratio: 5.142 Gaps: 0  
 Percent Similarity: 98.446 Percent Identity: 96.373

alignment\_block:

US-09-155-327E-9 x AX030819 ..  
 Align seg 1/1 to: AX030819 from: 1 to: 581

1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17  
 |||||  
 1 ATGCGGACCCCAAGCTCAACCCACACACACGCGCTAGTGGCTGACTT 50

seq\_name: gb\_pr:CNS00008

seq\_documentation\_block:

LOCUS CNS00008 196292 bp DNA linear PRI 22-MAY-2001  
 DEFINITION Human chromosome 14 DNA sequence BAC R-124D2 of library RpCl-11  
 from chromosome 14 of Homo sapiens (Human), complete sequence.  
 ACCESSION AL049829  
 VERSION AL049829.4 GI:8217859  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS

1 (bases 1 to 196292)  
 Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.  
 Heilig,R., Petrij,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,  
 Brothier,P., Catillo,L., Barde,V., Pelletier,E., Attienave,F.,  
 Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C.,  
 Gyapay,G., Saurin,W. and Weissenbach,J.  
 Sequencing of the human chromosome 14

JOURNAL

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL

COMMENT

On Jun 3, 2000 this sequence version replaced gi:6138746.  
 ----- Genome Center  
 Center: GenomeScope / Centre National de Sequencage

Center code: GS  
Web site: <http://www.genoscope.cns.fr/>  
Contact: [SeqRef@genoscope.cns.fr](mailto:SeqRef@genoscope.cns.fr)

The following BAC sequence is oriented from the T7 to the SP6 end.  
Upstream BAC (overlapping the T7 end) : R-244E17  
Downstream BAC (overlapping the SP6 end) : C-2201G16 (AC-AL132855)  
Summary Statistics

Assembly program: Phrap; version 2.0  
Quality coverage: 7.94x in Q20 bases; sum-of-coverage

# Overall quality chart :

```

Range      : bases
1 - 9      :
10 - 19    :
20 - 29    : 10
30 - 39    : 30
40 - 49    : 829
50 - 59    : 1909
60 - 69    : 5193
70 - 79    : 18093
80 - 89    : 58972
90 - 99    : 111256

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Percentage of bases with a quality value >= 40 : 99 %.

## Location/Qualifiers

1. 196292

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/chromosome="14"

/clone="R-124D2"

/clone\_11b="R-PCR-11"

/note="matching EMBL:R9102162"

RHdb:RH102162

dbSTS:STS69699

Identified using the e-PCR software (G. Schuler)"

80433. 80566

/note="matching EMBL:AA167748"

RHdb:RH98727

dbSTS:STS68485

Identified using the e-PCR software (G. Schuler)"

82164. 82299

/note="matching EMBL:H79035"

RHdb:RH78773

dbSTS:STS3514

Identified using the e-PCR software (G. Schuler)"

93580. 93808

/note="matching EMBL:AA007328"

RHdb:RH75103

dbSTS:STS52191

Identified using the e-PCR software (G. Schuler)"

107758. 107951

/note="matching EMBL:R94929"

RHdb:RH65111

dbSTS:STS45044

Identified using the e-PCR software (G. Schuler)"

107996. 108181

/note="matching EMBL:D11677"

RHdb:RH47139

dbSTS:STS40201

Identified using the e-PCR software (G. Schuler)"

128387. 128525

/note="matching EMBL:R22648"

RHdb:RH53520

dbSTS:STS25817

Identified using the e-PCR software (G. Schuler)"

128419. 128543

/note="matching EMBL:R87257"

RHdb:RH53698

dbSTS:STS18321

STS

Identified using the e-PCR software (G. Schuler)"

138462. 138738

/note="matching EMBL:R59134"

RHdb:RH53972

dbSTS:STS42930

Identified using the e-PCR software (G. Schuler)"

138509. 138658

/note="matching EMBL:M78864"

RHdb:RH95543

RHdb:RH1243

dbSTS:STS24710

Identified using the e-PCR software (G. Schuler)"

138568. 138647

/note="matching EMBL:M78986"

RHdb:RH28416

dbSTS:STS20162

Identified using the e-PCR software (G. Schuler)"

138568. 138677

/note="matching EMBL:M78946"

RHdb:RH28671

dbSTS:STS20163

Identified using the e-PCR software (G. Schuler)"

138805. 138926

/note="matching EMBL:H72023"

RHdb:RH68657

dbSTS:STS48564

Identified using the e-PCR software (G. Schuler)"

161617. 161761

/note="matching EMBL:AA452257"

RHdb:RH92419

dbSTS:STS65422

Identified using the e-PCR software (G. Schuler)"

194804. 194903

/note="matching EMBL:N91549"

RHdb:RH76320

dbSTS:STS53407

Identified using the e-PCR software (G. Schuler)"

50870 a 45673 c 47123 g 52626 t

BASE COUNT

ORIGIN

alignment\_scores:

Quality: 863.50 Length: 399

Ratio: 4.474 Gaps: 2

Percent Similarity: 48.371 Percent Identity: 47.118

alignment\_block:

US-09-155-327E-9 x CNS00008 ..

Align seg 1/1 to: CNS00008 from: 1 to: 196292

1 MetAlaThrProAlaSerThrProAspThrArgAlaValAlaAspPh 17

89826 ATGGGACCCGACGCTCGGGCCGACGACGCTGCTGGGACGCTT 89875

17 eValGlyTyrArgLeuArgGlnGlyTyrValCysGlyAlaGlyProG 34

89876 TGTAGGTATTAAGCTGAGCAGAGGTTATGCTGTGAGACTGGCCCG 89925

34 lYsGlnGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaGly 50

89926 GGGAGGCGCCGACGCTGACCGCTGACCAAGCCATGCGGCGAGTGA 89975

51 AspGluPheGluThrArgPheArgThrPheSerAspLeuAlaAlaG 67

89976 GATGAGTTGAGACCCGCTTCGCGGCGACCTTCTGATCTGGCGGCTCA 90025

67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSer 84

90026 GCTGATGTGACCCGACGCTGACCCGACCAAGCCTTCAACCGAGTCTCG 90075

84 SpGluLeuPheGlnGlyProAsnTrpGlyArgLeuValAlaPhePhe 100

90076 ATGAACCTTTTTCAGGGGGCCCCCAACTGGGGCCGCTTGTAGCCTTCTT 90125  
 101 VALPheglYAlaAlaLeuCYsAlaGlnSerValAsnLYsGluMetGluP 117  
 10126 GTCTTTGGGGCTGCACCTGTGTCTGAGAGTGTCAACAAGGAGATGGAACC 90175  
 117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGlnPheArgL 134  
 90176 ACTGGGGGACACAGTCAGAGTGGTGGCTTACTCTGAGAGACGAC 90225  
 134 euAlaSprPrlLeHisSerSerGlyGlyTrp..... 144  
 90226 TGGCTGACTGTGATCCACAGCAGTGGGGCTGGGTAAAGACTTTCATTT 90275  
 144 ..... 144  
 90276 GCCGCTTCACATCCTTTCGAAAGCTGTCTCCAGGGGGAAAGATGGGG 90325  
 144 ..... 144  
 90326 GCTCTGATTGGAGGCTGAGGACGATGTTGGGATGAGTACGGGGCTG 90375  
 144 ..... 144  
 90376 AGTCTCCCGCTTGATGGAATTAGATTGAGAGATCCTGGACTTCAC 90425  
 144 ..... 144  
 90426 TCCAGGGCTGCATGACGATCAACACTGGATGGCTCATGGTCCCAAGCAG 90475  
 144 ..... 144  
 90476 AGGACAGATACACACCCAAAGAGTGCCTCAGGGGAATTGTCTCAGGGA 90525  
 144 ..... 144  
 90526 CTTTTCATCTGAGTCATGGCGTGGAGAGTGGGGAGACGAGGATGGG 90575  
 144 ..... 144  
 90576 TGGGTGTCAGCAAGCCTTGGCAAGGATGCTAGTTCTGAGCAGAAATTTT 90625  
 144 ..... 144  
 90626 TCGCCAGGAAAGATGGAATTCACCTGAGGACAGAGTGGGCAATGAACC 90675  
 144 ..... 144  
 90676 AGTCTCTCAGGGTGGGGTGCACCTGGGGGATGAGAGGGCTTGCAGGG 90725  
 144 ..... 144  
 90726 AGAAGAGCTTTGGCCAGAGAGAGCTGGGTATGGGTGTCTGCGCACTG 90775  
 144 ..... 144  
 90776 GATGGAACGTGAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 90825  
 145 ..... Ala 145  
 90826 GATATCCCTTTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 90875  
 146 .GluPheThrAlaLeuTyrGlyAspGlyAlaLeuGlnGluAlaArgArgL 162  
 90876 GGAGTTACAGCTCTATACGGGAGCGGGCCCTGGAGAGCGCGCGCTG 90925  
 162 euArgGluGlyAsnTrpAlaSerValArgThrValLeuThrGlyAlaVal 178  
 90926 TCGCGGAGGGGAACTGGGCAATCAGTGAAGACATGCTGAGGGGGCCGTG 90975  
 179 AlaLeuGlyAlaLeuValThrValGlyAlaPhePheAlaSerLYs 193  
 90976 GCACCTGGGGGCGCTGTACTGTAGGGGCTTTTGTCTAGCAAG 91020

seq\_name: gb.htg:AC079885

seq\_documentation\_block: 151212 bp DNA linear HTG 08-NOV-2000

LOCUS AC079885 Rattus norvegicus chromosome 4 clone RP31-246H8 strain Brown

DEFINITION Norway, WORKING DRAFT SEQUENCE, 5 unordered pieces.

ACCESSION AC079885.2 GI:11120768

VERSION AC079885.2 HTG: HTGS\_PHASE1: HTGS\_DRAFT.

KEYWORDS HTG: HTGS\_PHASE1: HTGS\_DRAFT.

SOURCE Norway rat.

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus

1 (bases 1 to 151212)

REFERENCE 1 (bases 1 to 151212)

AUTHORS Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W.,

Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Gupta, J.,

Ho, S.-L., Idol, J., Karlins, E., Lee-Hin, S.-Q., Legaspi, R., Lim, M.,

Maduro, O.L., Maduro, V.B., Mastrian, S.D., McCloskey, J.C.,

McDowell, J., Pearson, R., Prasad, A., Snyder, B., Stantip, S.,

Thomas, J.W., Thomas, P.J., Tjongson, E.E., Touchman, J.W.,

Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D. and Green, E.D.

Unpublished

2 (bases 1 to 151212)

REFERENCE 2 (bases 1 to 151212)

AUTHORS Direct Submission

TITLE Submitted (16-SEP-2000) NIH Intramural Sequencing Center, 8717

JOURNAL Groveomont Circle, Gaithersburg, MD 20877, USA

COMMENT On Nov 8, 2000 this sequence version replaced gi.10179358.

----- Genome Center

Center: NIH Intramural Sequencing Center

Center code: NISC

Web site: http://www.nisc.nih.gov

Contact: nisc.mouse@nih.gov

----- Project Information

Center project name: rk

Center clone name: 246H8

----- Summary Statistics

Sequencing vector: plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 147800 bases at least Q40

Consensus quality: 149333 bases at least Q20

Insert size: 145000; agarose-fp

Insert size: 150812; sum-of-contigs

Quality coverage: 11.76x in Q20 bases; sum-of-contigs

Quality coverage: 11.30x in Q20 bases; sum-of-contigs

-----

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 5 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as

\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will

\* be preserved

1 20440: contig of 20440 bp in length

20540: gap of unknown length

20541 41009: contig of 20469 bp in length

41010 41109: gap of unknown length

41110 65552: contig of 24443 bp in length

65553 65652: gap of unknown length

65654 110365: contig of 44713 bp in length

110366 110465: gap of unknown length

110466 151212: contig of 40747 bp in length.

151212: contig of 40747 bp in length.

Location/Qualifiers

1. 151212

/organism="Rattus norvegicus"

/strain="Brown Norway"

/db\_xref="taxon:10116"

FEATURES

source

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misc_feature      /chromosome="4"
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                  20541..41009
                  /note="assembly_fragment"
                  /clone_end="T7"
misc_feature      /note="assembly_fragment"
                  /vector_side="left"
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misc_feature      /note="assembly_fragment"
BASE COUNT      43370 a 30838 c 31177 g 45417 t 410 others
ORIGIN

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alignment_scores:
  Quality: 674.00      Length: 193
  Ratio: 4.036        Gaps: 1
  Percent Similarity: 86.528  Percent Identity: 69.948

alignment_block:
  US-09-155-327e-9 x AC079885 ..
  Align seg 1/1 to: AC079885 from: 1 to: 151212

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1 MetlaarhPrroAlaAlaAspProLeuHISGlnAlaMetarGalaAlaGly 17
74558 ATGGCAACCCCAACCTTAATCCAGACACATGGGCTCTAATGGTGA... 74604
17 evalGlyTyArgLeuArgGlnIysGlyTyValGlySGLValGlyProg 34
74605 .....GCTGGCCCCG 74614
34 LyGlnGlyProAlaAlaAspProLeuHISGlnAlaMetarGalaAlaGly 50
74615 GGGAGAGCCCAACACCTGATACACCAACCATGGGCTGCTGCA 74664
51 AspGluPheGlnThrArgPheArgThrPheSerAspLeuAlaAlaGly 67
74665 GACAAAGTTAAGACCCATCCAGCACACCTTCTGACCTGCGCACTCA 74714
67 nleuHISValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
74715 GCTACATGTGATGCCAGGCTCAGCCCAACATGCTTCAACCCAGTTTCCA 74764
84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaAlaPhe 100
74765 ACAAACTTTTCCAAAGGGGCCCCCAACTAGGGCCATCTGTGACATCTTT 74814
101 ValPheGlyAlaAlaLeuGlySGLValSerValAsnIysGlnMetGluPr 117
74815 GTCCTTGGGGCTGCTGCTGCTGAGAGTGCACAGAAAATAGAGCC 74864
117 oleuValGlyGlnValGlnAspTrpMetValAlaArgLeuGlnThrArgL 134
74865 ATTGGTGGGCAAGTGCAGGATGGATGGTCCACCAAGACAGCC 74914
134 euAlaAspTrpIleHisSerGlyGlyTyArgLeuGlnPheThrAlaLeu 150
74915 TGGCTGACGTGATCCAAACATGGGGCTGGTGGAGATTCCAGCTCTA 74964
151 TyArgIysAspGlyAlaLeuGlnGlnAlaArgArgLeuArgGlnIysAsnTr 167
74965 TTCGGGAATGGGGCCCTAGAAAGACATGCTGAGGGGAGGAGACTG 75014
167 palAsSerValArgThrValLeuThrGlyAlaValAlaLeuGlnIysAlaLeu 184

```

```

75015 GGCATCAGTAGAGCAATACGTACTGGGCTGTGACATCGGACCTGA 75064
184 alThrValGlyAlaPhePheAlaSerIys 193
75065 TAACGTGAAGGGCCCTTTTACTAACAAG 75093
seq_name: gb_hhg:AC084240

```

```

seq_documentation_block:
  LOCUS      AC084240      181282 bp      DNA      linear      HTG 18-OCT-2000
  DEFINITION Rattus norvegicus chromosome 4 clone RP31-103121 strain Brown
  ACCSSION   AC084240
  VERSION    AC084240.1 GI:10864175
  KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT.
  SOURCE     Norway rat.
  ORGANISM   Rattus norvegicus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
             Rattus.

```

```

REFERENCE
  1 (bases 1 to 181282)
  Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W.,
  Bouffard, G.G., Brinkley, C., Dietrich, N.L., Gupta, J., Ho, S.-L.,
  Idol, J., Lee-Lin, S.-O., Legaspi, R., Lim, M., Maduro, Q., L.,
  Maduro, V.B., Mastrian, S.D., McCloskey, J.C., McDowell, J.,
  Pearson, R., Prasad, A., Snyder, B., Stantirpop, S., Thomas, J.W.,
  Thomas, P.J., Tjongson, E.E., Touchman, J.W., Tyan, J.T., Tsurgon, C.,
  Vogt, J.L., Walker, M.A., Welchby, K.D. and Green, E.D.
  NISC Mouse Sequencing Initiative
  Unpublished
  2 (bases 1 to 181282)
  Green, E.D.
  Direct Submission
  Submitted (18-OCT-2000) NIH Intramural Sequencing Center, 8717
  Grovemont Circle, Gaithersburg, MD 20877, USA
  ----- Genome Center
  Center: NIH Intramural Sequencing Center
  Center code: NISC
  Web site: http://www.nisc.nih.gov
  Contact: nisc.mouse@hgti.nih.gov
  ----- Project Information
  Center project name: r1
  Center clone name: 103121

```

## COMMENT

```

----- Summary statistics
Sequencing vector: plasmid; n/a; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 179798 bases at least Q40
Consensus quality: 180132 bases at least Q30
Consensus quality: 180274 bases at least Q20
Insert size: 138000; agarose-fp
Insert size: 160000; pulse-field-gel
Insert size: 180982; sum-of-contigs
Quality coverage: 15.02x in Q20 bases; agarose-fp
Quality coverage: 12.95x in Q20 bases; pulse-field-gel
Quality coverage: 11.45x in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

```

1 5430: contig of 5430 bp in length
* 5530: gap of unknown length
* 5531 39503: contig of 33973 bp in length
* 39504 39603: gap of unknown length
* 39604 85792: contig of 46189 bp in length
* 85793 85892: gap of unknown length
* 85893 181282: contig of 95390 bp in length.
Location/Qualifiers

```

## FEATURES

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source
1. .181282
/organism="Rattus norvegicus"
/strain="Brown Norway"
/db_xref="taxon:10116"
/chromosome="4"
/clone="RP31-103121"
/clone_id="RP31"
1. .5430
/note="assembly_fragment"
clone_end:SP6
vector_side:right"
5531..39503
/note="assembly_fragment"
clone_end:T7
vector_side:left"
39604..85792
/note="assembly_fragment"
85893..181282
/note="assembly_fragment"

misc_feature
misc_feature
misc_feature
BASE COUNT 50811 a 36290 c 37296 g 56560 t 325 others
ORIGIN

alignment_scores:
Quality: 674.00 Length: 193
Ratio: 4.036 Gaps: 1
Percent Similarity: 86.528 Percent Identity: 69.948

alignment_block:
US-09-155-327E-9 x AC084240 ..

Align seg 1/1 to: AC084240 from: 1 to: 181282

1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
|||||.....:|||||.....:
49782 ATGGCAACCCCACTCAATCCAGACACATGGCTTAATGTTGA... 49828

17 eValGIYTYrArgLeuArgInLysGIYTYrValCysGIYrArg 34
|||||.....:|||||.....:
49829 .....GCTGGCCCCG 49838

34 IyGIuGIYProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
|||||.....:|||||.....:
49839 GGGAGAGCCCAACACCTGATACACCAAGCATGTGGCTGCTGA 49888

51 AspGIuPheGIuThrArgPheArgThrPheSerAspLeuAlaAlaGI 67
|||||.....:|||||.....:
49889 GACAACTTAGACACCCACTTCCAGACACCTCTGACCTGGCCACTCA 49938

67 nLeuHisValThrProGlySerAlaGlnInArgPheThrGlnValSerA 84
|||||.....:|||||.....:
49939 GCTACATGTGTGCCAGGCTCCAGCCCAACAATGTTTACCCAGTTTCCA 49988

84 spGIuLeuPheGlnGIYrProAsnTrpGIYrArgLeuValAlaPhePhe 100
|||||.....:|||||.....:
49989 ACGAACTTTTCCAAAGGGGGCCCAACTAGGGCCATCTTGTGACATCTTT 50038

101 ValPheGIYAlaAlaLeuGlyAlaGluSerValAsnLysGIuMetGluPr 117
|||||.....:|||||.....:
50039 GTCCTTGGGGCTGCCGTGTGTGTGAGAGTGTACAGAAAATAGAGACC 50088

117 oLeuValGIYGIYAlaGlnAspTrpMetValAlaTyrLeuGIuThrArgL 134
|||||.....:|||||.....:
50089 ATTGTTGGAGACAGTGCAGATGTGATGTGTGCTTACCCAGACAGACGCC 50138

134 euAlaAspTrpIleHisSerGIYrGIYrAlaGluPheThrAlaLeu 150
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50139 TGGCTGACTGATCCACAAATAGGGGCTGTGTGAGTTTCCAGCTCTA 50188

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Thu Jun 6 16:39:21 2002

us-09-155-327e-7.p2n.rml

Page 1

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Date: Jun 6, 2002 2:32 PM  
About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

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Sequence 2, Application US/08798897  
Patent No. 5789201  
GENERAL INFORMATION:  
APPLICANT: Gastelella, John  
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
TITLE OF INVENTION: Homologue  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08798,897  
FILING DATE: February 11, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1483,0140001  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 579 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: CDNA  
US-08-798-897-2

alignment\_scores: Length: 193  
Quality: 1002.00 Gaps: 0  
Ratio: 5.219  
Percent Similarity: 99.482 Percent Identity: 99.482

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; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483, 0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-08-978-523-2

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  Ratio: 5.219          Gaps: 0
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seq_documentation_block:
; Sequence 1, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John

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TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2  
 TITLE OF INVENTION: Homologue  
 NUMBER OF SEQUENCES: 53  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 STREET: 1100 New York Avenue, N.W., Suite 600  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/798,897  
 FILING DATE: February 11, 1997  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Esmond, Robert W.  
 REGISTRATION NUMBER: 32,893  
 REFERENCE/DOCKET NUMBER: 1483.0140001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-2540  
 TELEFAX: 202-371-2600  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 579 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: both  
 MOLECULE TYPE: cDNA  
 US-08-798-897-1

alignment\_scores:  
 Quality: 996.00 Length: 193  
 Ratio: 5.161 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 98.446

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seq\_documentation\_block:  
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Patent No. 5883229

GENERAL INFORMATION:

APPLICANT: Guastella, John

TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 New York Avenue, N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/978,523

FILING DATE: herewith

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/798,897

FILING DATE: February 11, 1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 1483.0140002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 579 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: cDNA

US-08-978-523-1

alignment\_scores:  
 Quality: 996.00 Length: 193  
 Ratio: 5.161 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 98.446

## alignment\_block:

US-09-155-327E-7 x US-08-978-523-1

Align seg 1/1 to: US-08-978-523-1 from: 1 to: 579

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17 ValGlyTyrLeuArgGlnGlyTyrValCysGlyAlaGlyProG 34
1 TTAGGCTATTAAGCTGACACAGAGGTTATGCTGTGGAGTGGCTG 100
34 LysIleuLysProAlaAlaAspProLeuHisGlnAlaMetArgAlaGly 50
101 GGGAGAGCCGACGACGACGCGCTGACACAGCCATGCGGGCAGCTGGA 150
51 AspgLysPheGlnThrArgPheArgThrPheSerAspLeuAlaAlaG 67
151 GACGAGCTTGACACCGGCTCCGGGCGACCTTCTGTGACCTGGCGCTCA 200
67 LeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSer 84
201 GCTACACGTCGACCCGACGCTGACGACCAAGCTTCAACCGAGTTTCCG 250
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101 ValPheGlyAlaAlaLeuCysAlaGlnSerValAsnLysGlnMetGlnP 117
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151 TyrGlyAspGlyAlaLeuGlnGlnAlaArgArgLeuArgGlnGlyAsnTr 167
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167 PalaSerValArgThrValLeuThrGlyAlaValAlaLeuGlnAlaLeu 184
501 GGCATCAGTAGAGAGAGTGTGACGGGGGCTGTGGACATGGGGGCGCTGG 550
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seq\_name: /cgn2/6/ptodata/1/ina/5A\_COMB.seq: US-08-081-448-5

## seq\_documentation\_block:

Sequence 5, Application US/08081448

Patent No. 5646008

GENERAL INFORMATION:

APPLICANT: Thompson, Craig B.

APPLICANT: Boise, Lawrence H.

TITLE OF INVENTION: Vertebrate Apoptosis Gene:

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESS: Arnold, White &amp; Durkee

STREET: 321 No. 5646008th Clark Street, Suite 800

CITY: Chicago

STATE: IL

COUNTRY: USA

ZIP: 60610

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/081,448
FILING DATE: 19930622
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646008thrup, Thomas E.
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-744-0090
TELEFAX: 312-755-4489
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 135..836
US-08-081-448-5

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## alignment\_scores:

Quality: 428.50 Length: 224  
 Ratio: 3.018 Gaps: 4  
 Percent Similarity: 63.393 Percent Identity: 40.625

## alignment\_block:

US-09-155-327E-7 x US-08-081-448-5

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27 r..... 27
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28 .....ValCysGlyAlaGlyPro 33
250 AAGGAGTGAATGGAGATGGAGACCCCGCATGCAATGCAACCA 299
34 .....GlyGlnGlyProAlaAlaAsp..... 40
300 TCCTGGACCTGGCAGACAGCCCCGGGTGATGAGAGGACATGCGCACAG 349
41 .....ProLeuHisGlnA 45
350 CACGACTTGGATGCCCGGAGAGTATGCCCATGGCAGACAGTAAGCAAG 399
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78 gPheThrGlnValSerAspGlnLeuPheGlnGlyLysProAsnTrpGly 95
500 CTTGAACAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 549
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; Patent No. 5834309
; Patent No. 5834309 5710045
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.
; APPLICANT: Boise, Lawrence H.
; TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,670A
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,448
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARCD:090--1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135..836
; US-08-470-670A-6

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alignment\_scores:  
Quality: 428.50  
Ratio: 3.018

Length: 224  
Gaps: 4

Percent Similarity: 63.393 Percent Identity: 40.625  
alignment\_block:  
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162 LeuArgGlu.....GlyAsnTrpAlaSerValArgThrValLeuThrGl 176
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seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-481-739-1
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; Sequence 1, Application US/08481739
; Patent No. 6143291
; GENERAL INFORMATION:
; APPLICANT: June, Carl H. and Thompson, Craig B.
; TITLE OF INVENTION: METHODS FOR ENHANCING T CELL SURVIVAL
; TITLE OF INVENTION: BY AUGMENTING BCL-XL PROTEIN LEVELS
; NUMBER OF SEQUENCES: 4

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CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,739
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,518
FILING DATE: 04-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A. (GAD)
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: RPI-034CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 135..836
US-08-481-739-1

alignment_scores:
Quality: 428.50 Length: 225
Ratio: 3.105 Gaps: 4
Percent Similarity: 61.333 Percent Identity: 41.333

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|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 547
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seq_documentation_block:
; Sequence 1, Application US/09167921A
; Patent No. 6172216
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Nickoloff, Brian J.
; APPLICANT: Zhang, Qiongling
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
; FILE REFERENCE: ISPI-0324
; CURRENT APPLICATION NUMBER: US/09/167,921A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)..(836)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: L20121 Genbank
; DATABASE ENTRY DATE: 1994-07-26
US-09-167-921-1

alignment_scores:
Quality: 428.50 Length: 224
Ratio: 3.018 Gaps: 4
Percent Similarity: 63.393 Percent Identity: 40.625

alignment_block:
US-09-155-327e-7 x US-09-167-921-1 ..
Align seg 1/1 to: US-09-167-921-1 from: 1 to: 926

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27 r..... 27
200 CAGCTGAGCTGATTAGTGTGGAAAGAACAGAGCTAGGCCCCAG 249
28 ..... ValCysGlyAlaGlyPro 33
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34 ..... GlyGlyGlyProAlaAlaASP..... 40
300 TCCTGGACCTGGCAGACAGCCCCGGGTGATGGAGCCACCTGCCACAG 349
41 ..... ProLeuHisGlnA 45
350 CAGCAGTTGGATGCCGGGAGGTGATCCCATGCGCAGCAGTAAACCAAG 399
45 lametargAlaAlaGlyAspGluPheGluThrArgPheArgThrPhe 61
400 CGCTGAGGAGGAGCGAGCGAGAGTTGAACTGGTACCGCGGGCATTC 449
62 SerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGlnar 78
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; Sequence 39, Application US/09277020
; Patent No. 6210892
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation
; FILE REFERENCE: ISPH-0339
; CURRENT APPLICATION NUMBER: US/09/277,020
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 09/167,921
; EARLIER FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: patentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 926
; TYPE: DNA

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; ORGANISM: Homo sapiens
; US-09-277-020-39

alignment_scores:
  Quality: 428.50      Length: 224
  Ratio: 3.018        Gaps: 4
  Percent Similarity: 63.393      Percent Identity: 40.625

alignment_block:
US-09-155-327E-7 x US-09-277-020-39 ..
Align seq 1/1 to: US-09-277-020-39 from: 1 to: 926

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27 r..... 27
200 CAGCTGAGTGCATTAGTGTGGAAAGAACAGAGCTAGGCCCCAG 249
28 ..... ValCysGlyAlaGlyPro 33
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45 lametargAlaAlaGlyAspGluPheGluThrArgPheArgThrPhe 61
400 CGCTGAGGAGGAGCGAGCGAGAGTTGAACTGGTACCGCGGGCATTC 449
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; Sequence 1, Application US/09323743
; Patent No. 6214986
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Nickoloff, Brian J.
; APPLICANT: Zhang, Qingling
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
; FILE REFERENCE: ISPH-0368
; CURRENT APPLICATION NUMBER: US/09/323,743
; EARLIER FILING DATE: 1999-05-01
; EARLIER APPLICATION NUMBER: 09/277,020
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 09/167,921
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)..(836)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: L20121 Genbank
; DATABASE ENTRY DATE: 1994-07-26
; US-09-323-743-1

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alignment_scores:
  Quality: 428.50      Length: 224
  Ratio: 3.018        Gaps: 4
  Percent Similarity: 63.393  Percent Identity: 40.625

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alignment_block:
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Align seg 1/1 to: US-09-323-743-1 from: 1 to: 926

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250 AAGGACTGAATCGGAGATGGAGACCCCGAGTGCATCATGACACCA 299
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34 .....GlyGlyProAlaAlaSp..... 40
300 TCCCTGGACCTGGACAGACGCCCGGCTGATGAGACCACTGGCCAG 349
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350 CAGCAGTTTGGATGCCGGGAGATGATCCCATGCGACGACTAAGCAG 399
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450 AGTACCTGACATCCAGTCCATCACCACCGGAGGAGGAGGAGGAGGAG 499
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78 gPheThrGlnValSerAspGlnLeuPheGlnGlyProAsnTrpGlyA 95
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500 CTTTGAACAGAGTATGATGATGATGATGATGATGATGATGATGATGAT 549

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95 rgleuValAlaPhePheValPheGlyAlaAlaLeuCysAlaGluSerVal 111
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550 GCATTGTGGCTTTCTCTCTCGGGGCGACCTGTGGTGAAGCGTA 599
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650 TTAACCTGATGACGACCTAGAGCCCTGATGATGATGATGATGATGAT 699
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162 LeuArgGlu.....GlyAsnTyrPheSerValArgThrValLeuThrG 176
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750 GCCAGGAGACGCTTCACCGCTGCTGCTGATGATGATGATGATGATGAT 799
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seq_name: /cgn2.6/ptodata/1/ina/6B.COMB.seq:US-08-461-511A-6

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seq_documentation_block:
; Sequence 6, Application US/08461511A
; Patent No. 6303331

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; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.B.
; TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE COMPOSITIONS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESS: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,511A
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: UNKNOWN
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARCD:179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135..836
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-461-511A-6

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US-09-155-327E-7  
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in seg 1/1 to: US-08-461 222

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11 ArgalateValAlaAspheValGlyTyrLysLeuArgGlnLysGlyIle 199  
||| ||||||||| ||||||||| ||||||||| |||||||||  
150 CGGAGCTGGTGTCATTCTCCACAAAGCCTTCCCAAGAATG 27

27 T..... 249  
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 200 CAGCTGAGACAGTTTACTGATGTGAGAACGACAGACTGTGAGCCCCAG 33  
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28 .....::: 299
250 AACGGACTGATCGAGATGGAGACCCCGATGCCATCAATGGCAACCA 40
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[illegible]

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78 gpherhrgInValSeraspGlutLeupheGlnGlyVal<sup>20</sup>  
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500 CMTTGACAGGTGATGAATGAACCTTCGGATGGGGTAACTCGGGC  
GCAAGLISerVal<sup>1</sup>

95 rgLeuValAlaPhepheValpheGlyAlaIalaLeucysalio  
|:::||||||| |:::|||||||:::|||||||  
550 GCATTGTGGCCTTTTCCTCCTCGGCCGGSGACACTGTGCCTGGAAAGCGTA  
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; Sequence 6, Application PC/TUS9407089.
; GENERAL INFORMATION:
; IMPORTANT:
; Note: Extrachromosomal Apoptosis Gene:
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APPLICANT: Verbovetskiy  
TITLE OF INVENTION: Compositions and Methods  
TITLE OF INVENTION:  
TITLE OF INVENTION:  
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
Box 443

STREET: P.O. Box 4444  
CITY: Houston  
STATE: TX  
COUNTRY: United States of America

ZIP: 77210  
COMPUTER READABLE FORM:  
COMPUTER TYPE: Floppy disk  
MEDIUM TYPE: IBM PC compatible  
COMPUTER: IBM PC compatible  
OS: MS-DOS

COMPUTER SYSTEM: PC-DOS/MS-DOS  
OPERATING SYSTEM: PC-DOS/MS-DOS  
CURRENT APPLICATION NUMBER: PCT/US94/070  
APPLICATION NUMBER: CONCURRENTLY FILED  
FILING DATE:

CLASSIFICATION: 08/081.448  
PRIORITY APPLICATION NUMBER: 08/081.448  
APPLICATION DATE: 22 JUNE 1993

FILING DATE: 11/11/2011  
 ATTORNEY/AGENT INFORMATION:  
 NAME: PARKER, David L.  
 REGISTRATION NUMBER: 32,165  
 REGISTRATION DOCKET NUMBER: ARCD09

REFERENCE/DOCUMENT INFORMATION:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512-320-7200  
TELEFAX: 713-789-2679  
FACSIMILE: 713-789-2679

INFORMATION FOR SEQUENCE CHARACTERISTICS:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 926 base pairs  
 TYPE: nucleic acid

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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE:

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RELATION:	CDS
NAME/KEY:	135..836
LOCATION:	
PCT-US94-07089-6	

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alignment_scores: 428.50
quality: 3.105
ratio:
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Percent Similarity: 61.333 Percent

US-09-155-32/E-1  
Align seg 1/1 to: PCT-US94-07089-

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27 T.....  
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200 CAGCTGAGTCAGTTAGTGATGTG

27 .....  
250 AAGGACTGAATCGGAGATGGAGAC

28 .....  
300 TCCTGGCAGCTGGCAGACAGCCCC

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35  uGlyProAlaAlaSP.....
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347  CAGCAGCAGTTTGATGCCCGGG

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44 InAlaMetArgAlaAlaGlyAsp  
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397 AAGCGTGAGGAGGAGCGCGAC

61 pheSerAspLeuAlaGlnLe

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Page 9

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447 TTTCAGTACCTGACATCCAGCTCCACATACCCAGGAGGACGATATCA 496
77 nargpethrlnValSeraspGluLeupheglnnglylProasnTrpG 496
497 GACCTTGAACAGAGTGAATGATACCTTCCGGGATGGGTAAACGCGG 94
94 lYarGLueValAlaPhepheValPheglYAlaAlaLeuCyAlaGluSer 546
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144 rPalAGluPheThrAlaLeuTyrglyAspGlyAlaAlaLeuGluAlaArg 696
697 GCGATACCTTTGTGGAACCTTATGGACATGCAAGCAGCGGAGAGCGA 746
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797 GGGCTGGTCTGCTGGGCTCACCTC 821

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seq_documentation_block:
; Sequence 20, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1735 S. Jefferson Davis Hwy., Suite 400,
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIORITY APPLICATION: 514
; APPLICATION DATA:
; FILING DATE: US 08/124,256
; PRIORITY APPLICATION DATA: 20-SEP-1993
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075

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/ INFORMATION FOR SEQ ID NO: 20:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 717 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ NAME/KEY: CDS
/ LOCATION: 1..717
/ US-08-465-485A-20

alignment_scores:
Quality: 410.50
Percent Similarity: 59.574
Length: 235
Gaps: 5
Percent Identity: 37.021

alignment_block:
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78 GGGCTGAGATGGATGGGAGATGAGGAGATGAGGAGGAGGAGGAGGAGG 127
33 .....ProGlyGlu..... 35
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35 ..... 35
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328 GCGCACTCCGAGATGTCACGCGACGCTGACCTGACGCGCTTACCGC 377
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428 ACTGGGAGAGATTTGGCTTTGACTTGGTGGGCTGATGCTGCTG 477
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478 GAGAGCGCTCAACCGGAGATGTCGCGCTGAGACACATCGCCCTGTG 527
125 pMetValAlaTrpLeuGluThrArgLeuAlaAspTrpIleHsserSerG 142
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: Sequence 20, Application US/09080285
: Patent No. 6040181
: GENERAL INFORMATION:
: APPLICANT: Reed, John
: TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
: NUMBER OF SEQUENCES: 29
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
: P.C.
: STREET: 1755 S. Jefferson Davis Hwy., Suite 400
: CITY: Arlington
: STATE: Virginia
: COUNTRY: U.S.A.
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/080,285
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/465,485
: FILING DATE: 05-JUN-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/124,256
: FILING DATE: 20-SEP-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/840,716
: FILING DATE: 21-FEB-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/288,692
: FILING DATE: 22-DEC-1988
: ATTORNEY/AGENT INFORMATION:
: NAME: Fortney, Andrew D.
: REGISTRATION NUMBER: 34,600
: REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (408) 436-2070
: TELEFAX: (408) 436-2075
: INFORMATION FOR SEQ ID NO: 20:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 717 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..717
: US-09-080-285-20

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alignment_scores:
: Quality: 410.50      Length: 235
: Ratio: 2.932        Gaps: 5
: Percent Similarity: 59.574      Percent Identity: 37.021

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378 GCGGAGACGCTTTCACCGGTGGAGAGACTTTCAGGAGCGGAGTGA 427
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seq_documentation_block:
: Patent No. 5459251
: APPLICANT: Tsujimoto, Yoshide, Croce, Carlo A.
: TITLE OF INVENTION: DNA MOLECULES HAVING HUMAN BCL-2 GENE
: SEQUENCES
: NUMBER OF SEQUENCES: 4

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Quality:	410.50	Length:	235
Ratio:	2.932	Gaps:	5
Percent Similarity:	59.574	Percent Identity:	37.021

Align seg 1/1 to: 5459251-1 from: 1 to: 4825

[illegible][illegible]







Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: <http://genome.gsc.riken.go.jp/>, Fax: 81-45-503-9216, Tel: 81-45-503-9222). Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Developmental Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGACAGCAGATCCAGCAAGACTCTTTTTCCTTTTTTTTAA 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGACAGCATTCGACGATTATTAATTAAATCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pluescript KS(+) after bulk excision from Lambda Fuc I. Cloning sites, 5' end; SalI, 3' end; BamHI. Host: DH10B.

Location/Qualifiers  
1 1949

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/sex="male"
/tissue_type="testis"
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132..713
CDS

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align seg 1/1 to: AK015644 from: 1 to: 1949

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34 LysGlnGlyProAlaIleAspProLeuHisGlnAlaMetArgAlaAlaGly 50  
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101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGlyupr 117  
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117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGlnLuphrArgL 134  
|||||  
482 TTTGGTGGGGCAAGTCACAGATTTGATGTGGCTTACTCTGAGAACACGTC 531  
134 euAlaAspTrpIleHisSerSerGlyGlyTyrAlaGluPheThrAlaLeu 150  
|||||  
151 TTYGlyASPlyAlaLeuGlnGluAlaArgArgLeuArgGlnLysAspTr 167  
|||||  
582 TAGGGGGAGGGGGCCCTGGAGGAGGCAAGGGGTCCTGGGGAGGGGAGACTG 631  
167 pAlaSerValArgThrValLeuThrGlyValAlaLeuGlyAlaLeuY 184  
|||||  
632 GGCATCAGTGAAGACAGTCGACGGGGGCCCTGGGCACTGGGGGCCCTTGG 681  
184 alThrValGlyAlaPhePheAlaSerLys 193  
|||||  
682 TTAAGTGAAGGCCCTTTTGTGCTAGCAAG 710

```

seq_documentation_block:
LOCUS AK004680 3487 bp mRNA HTc 19-JAN-2002
DEFINITION Mus musculus adult male lung cDNA, RIKEN full-length enriched
library, clone:1200009L24:Bc12-11ke 2, full insert sequence.
ACCESSION AK004680
VERSION AK004680.1 GI:12836027
KEYWORDS HTc; CAP trapper.
SOURCE Mus musculus (strain:C57BL/6J) adult male lung cDNA to mRNA,
clone:1ib:RIKEN full-length enriched mouse cDNA library
clone:1200009L24.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
METH. ENZYMOL. 303, 19-44 (1999)
JOURNAL MEDLINE 99279253
PUBMED 10349636
REFERENCE
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL MEDLINE 20499374
PUBMED 11042159
REFERENCE
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M.,
Yamamoto, R., Matsumoto, H., Sakaiguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Ogawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system—384-format
sequencing pipeline with 384 multicapillary sequencer

```





## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1030)  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: DCTD/DTP  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at: Image.llnl.gov  
Plate: L1C6M00 row: P column: 04  
High quality sequence start: 5  
High quality sequence stop: 709.  
Location/Qualifiers  
1. 1030

## FEATURES

source  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="NIH-MGC-7"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: lung; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; CDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAC(G). Size selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-CDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."  
BASE COUNT 190 a 284 c 386 g 170 t  
ORIGIN

## alignment\_scores:

Quality: 955.00 Length: 190  
Ratio: 5.080 Gaps: 1  
Percent Similarity: 98.947 Percent Identity: 97.368

## alignment\_block:

US-09-155-327e-7 x BE793530 ..

Align seg 1/1 to: BE793530 from: 1 to: 1030

```

1 MetAlaThPrOAlaSerAlaProAspRrArGaLaLeuValAlaAspPh 17
|||||
144 ATGGGACCCCAAGCCTCGGCCACACACGGGCTGTGGCAGACTT 193
17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyValGlyProg 34
|||||
194 TGTAGATTATAGCTGAGGAGGAGGTTATGTCTGTGGAGCTGGCCCCG 243
34 TGTAGGTTATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 243
|||||
244 GGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 293
51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaIagi 67
|||||
294 GATGAGTTGAGACCCGCTTCGGCAGCCTTCCTCATATGCGGCGCTCA 343
67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
|||||
344 GCTGATGTGACCCCAAGGCTGAGCCCAACACCTTCACCCAGGCTCCG 393
84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
|||||
394 ATGAACCTTTTCAAGGGGAGCCCAACTGGGAGGAGGAGGAGGAGGAGG 443

```

```

101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluP 117
|||||
444 GTCTTTGGGGCTGCACTGTCTGTCTGAGAGTGTCAACAAGGAGATGAAC 493
117 cLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArg 134
|||||
494 ACTGGTGGAGCAAGTGCAGAGTGTGATGTGGTCTGAGAGAGCGGC 543
134 eAlaAspTrpPheHisSerSerGlyTyrTrpAlaGluPheThrAlaLeu 150
|||||
544 TGGCTGACATGATCCACAGCAGTGGGCTGGCGGAGTTTCACAGCTCA 593
151 TyrGlyAspGlyAlaLeuGluGlnAlaArgArgLeuArgGlyAsnTr 167
|||||
594 TACGGGAGAGGGGCGCTGAGAGAGCGCGGCTGCGGGAGAGGAGCTG 643
167 pAlaSerValArgTrpValLeuThrGlyAlaValAlaLeuGlyAlaLeu 183
|||||
644 GGCATCACTGAGACACTGCTGACGGGGGCGGTGGCACTGGGGCGCTG 693
184 ValThrValGlyAlaPhe 189
|||||
694 GTAACGTGAGGGGCGCTTT 711

```

seq\_name: gb\_est:AL157542

seq\_documentation\_block:

LOCUS AL157542 804 bp mRNA linear EST 24-FEB-2000  
DEFINITION DKFZP761D0816\_r1 761 (synonym: hamy2) Homo sapiens CDNA clone  
AL157542  
VERSION AL157542.1 GI:7057943  
KEYWORDS EST.

## SOURCE

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 804)  
Ansoerge,W., Winkner,U., Mewes,W., Well,B. and Wiemann,S.  
EST (Ansoerge,W., Winkner,U., Mewes,W., Well,B. and Wiemann,S.)  
Unpublished (1999)  
Contact: Ansoerge W  
MIPS

Am Kioferspitz 18a D-82152 Martinsried, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;  
Heidelberg/Germany) within the CDNA sequencing consortium of the  
German Genome Project.  
No sl sequence available.

This clone (DKFZP761D0816) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY. Email: clone@rzpd.de.

## FEATURES

## source

1. 804  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="DKFZP761D0816"  
/clone\_lib="761 (synonym: hamy2)"  
/tissue\_type="amygdala"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Vector: pSport1; Site\_1: NotI; Site\_2: SalI"  
BASE COUNT 150 a 217 c 294 g 142 t 1 others  
ORIGIN

## alignment\_scores:

Quality: 953.00 Length: 193  
Ratio: 4.964 Gaps: 0  
Percent Similarity: 99.482 Percent Identity: 99.482

alignment block:  
US-09-155-327E-7 x AL157542

Align seg 1/1 to: AL157542 from: 1 to: 804

```

1  MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
   |||||||
134 ATGGGAGCCCGACCTCGGCCCGACAGACACGCGCTGGTGGAGACTT 183
   |||||||
17  eValGlyTyrIleuArgIleuGlyTyrValCysGlyAlaGlyProG 34
   |||||||
184 TGTAGGTTATAGCTGAGCGACAGAGGCTTATGCTGTGGAGCTGGCCCG 233
   |||||||
34  IyGlyGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaGly 50
   |||||||
234 GGGAGGCCCGACGAGCTGACCCGCTGACCAACCATGGGCGAGCTGA 283
   |||||||
51  AspGluPheGluThrArgPheArgThrPheSerAspLeuAlaAla 67
   |||||||
284 GATGAGTTCGAGACCCGCTTCGCGGACCTTCTCTGATCTGGCGCTCA 333
   |||||||
67  nLeuHisValThrProGlySerAlaGlnAlaArgPheThrGlnValSer 84
   |||||||
334 GCTGATGTGACCCGAGGCTCAGCCCAACAGCTTCACCCAGGCTCCG 383
   |||||||
84  SPGLuLeuPheGlnGlyIleProAsnTrpGlyArgLeuValAlaPhePhe 100
   |||||||
384 ATGAACTTTTCAGGGGGGCCCCCACTGGGGCCCTTGTAGCTTCTT 433
   |||||||
101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnIleGluMetGlu 117
   |||||||
434 GCTCTGGGGCTGCACTGTGTGCNAGAGTGTCAACAGAGATGGAAAC 483
   |||||||
117 OleuValGlyIleValGlnGluTrpMetValAlaTyrLeuGluThrArg 134
   |||||||
484 ACTGGTGGGACAAAGTGCAGAGAGTGTGAGTGTGAGTGTGAGAGCGCG 533
   |||||||
134 eValAspTrpIleHisSerSerGlyIleTyrPAlaGluPheThrAlaLeu 150
   |||||||
534 TGGCTGACAGATCCACAGCAGTGGGGGCTGGCGAGTTCACACTCTTA 583
   |||||||
151 TyrGlyAspGlyAlaLeuGluGluIleArgArgLeuArgGluGlyAsnTr 167
   |||||||
584 TACGGGAGCGGCCCTGGAGGAGCGCGCGCTCTCGGGAGGAGGAGCTG 632
   |||||||
167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeu 184
   |||||||
633 GGCATCTGAGGAGCAAGTGTGACGGGGCGCGGCACTT.GGGGCCCTGG 681
   |||||||
184 AlThrValGlyAlaPhePheAlaSerLys 193
   |||||||
682 TAACTGTAGGGGCTTTTGTGTAGCAAG 710

```

seq\_name: gb\_est2:BI770566

seq\_documentation block:

LOCUS BI770566 697 bp mRNA linear EST 25-SEP-2001  
DEFINITION 603060362F1 NIH\_MGC\_122 Homo sapiens cDNA clone IMAGE:5209862 5',  
mRNA sequence.

ACCESSION BI770566  
VERSION BI770566.1 GI:15762144

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 697)  
NIH-MGC <http://mgc.ncl.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [rgs@ncl.nih.gov](mailto:rgs@ncl.nih.gov)  
Tissue Procurement: Life Technologies, Inc.

# FEATURES

## source

CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNI)  
DNA sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LILNI at:  
<http://image.lnl.gov>  
Plate: LILNI526 row: k column: 15  
High quality sequence start: 21  
High quality sequence stop: 695.  
Location/Qualifiers

```

1..697
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5209862"
/clone_lib="NIH_MGC_122"
/lab_host="DH10B"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb. Insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."
BASE COUNT      121 a      202 c      248 g      126 t
ORIGIN

```

alignment scores:  
Quality: 890.00 Length: 187  
Ratio: 4.890 Gaps: 5  
Percent Similarity: 97.326 Percent Identity: 97.326

alignment block:  
US-09-155-327E-7 x BI770566

Align seg 1/1 to: BI770566 from: 1 to: 697

```

1  MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
   |||||||
145 ATGGGAGCCCGACCTCGGCCCGACAGACACGCGCTGGTGGAGACTT 194
   |||||||
17  eValGlyTyrIleuArgIleuGlyTyrValCysGlyAlaGlyProG 34
   |||||||
195 TGTAGGTTATAGCTGAGCGACAGAGGCTTATGCTGTGGAGCTGGCCCG 244
   |||||||
34  IyGlyGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaGly 50
   |||||||
245 GGGAGGCCCGACGAGCTGACCCGCTGACCAACCATGGGCGAGCTGA 294
   |||||||
51  AspGluPheGluThrArgPheArgThrPheSerAspLeuAlaAla 67
   |||||||
295 GATGAGTTCGAGACCCGCTTCGCGGACCTTCTCTGATCTGGCGCTCA 344
   |||||||
67  nLeuHisValThrProGlySerAlaGlnAlaArgPheThrGlnValSer 84
   |||||||
345 GCTGATGTGACCCGAGGCTCAGCCCAACAGCTTCACCCAGGCTCCG 394
   |||||||
84  SPGLuLeuPheGlnGlyIleProAsnTrpGlyArgLeuValAlaPhePhe 100
   |||||||
395 ATGAACTTTTCAGGGGGGCCCCCACTGGGGCCCTTGTAGCTTCTT 444
   |||||||
101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnIleGluMetGlu 117
   |||||||
445 GCTCTGGGGCTGCACTGTGTGTGAGAGTGTCAACAGAGATGGAAAC 494
   |||||||
117 OleuValGlyIleValGlnGluTrpMetValAlaTyrLeuGluThrArg 133
   |||||||
495 CACTGGTGGACAAAGTGCAGAGAGTGTGAGTGTGAGTGTGAGAGCGG 544
   |||||||
133 gLeuAlaAspTrpIleHisSerSerGlyIleTyrPAlaGluPheThrAla 150

```



```

/clone="IMAGE:5218294"
/clone_1lib="NHU_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH10B"
/notice="Vector: PCMV-SPORT6, Site_1: NotI, Site_2: EcoRV
(destroyed): RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:

```

seq.documentation.block:	815 bp	mus musculus	1 clone	EST 12-JUN-2001		
locus	BF785386	6021117282F1 NC1_CGAG_k1d14	mus musculus	IMAGE:4239798		
DEFINITION	5', mRNA sequence.					
ACCESSION	BF785386.1	GI:12090422				
VERSION						
KEYWORDS	EST.					
SOURCE	house mouse.					
ORGANISM	Mus musculus					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
REFERENCE	1 (bases 1 to 815)					
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .					
TITLE	National Institutes of Health. Mammalian Gene Collection (MGC)					
JOURNAL	Unpublished (1999)					
COMMENT	Contact: Robert Strausberg, Ph.D.					

\_\_\_\_\_





## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 758)  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Inqye Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
plate: L1AM1477 row: a column: 01  
High quality sequence stop: 753.

## FEATURES

## Source

Location/Qualifiers  
1..758  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5190792"  
/clone\_1lb="NIH\_MGC\_116"  
/lab\_host="DH10B"  
/note="Organ: pooled colon, kidney, stomach; Vector:  
PCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA  
source anonymous pool of 3 colons, age 26 yo male, 49 yo  
female, 71 yo male colon; 46 yo male kidney, and pool of 2  
stomachs, 62 yo male and 70 yo female. Library is  
oligo-dT primed and directionally cloned (EcoRV site is  
destroyed upon cloning). Average insert size 1.4 kb,  
insert size range 1-3 kb. Library is normalized and  
enriched for full-length clones and was constructed by C.  
Gruber (Invitrogen). Research Genetics tracking code  
023. Note: this is a NIH\_MGC Library."  
BASE COUNT 140 a 216 c 228 g 174 t  
ORIGIN

## alignment\_scores:

Quality: 583.00 Length: 112  
Ratio: 5.205 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 99.107  
alignment\_block:  
US-09-155-327e-7 x B1764428 ..

Align seg 1/1 to: B1764428 from: 1 to: 758

```

1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
|||||
139 ATGGCGACCCGACCTCGGCCGACACACGCGCTGCTGGCAGACTT 188
|||||
17 eValGlyTyrLeuArgGlnGlyTyrValCysGlyIaGlyProG 34
|||||
189 TGTAGCTTATAGCTGAGGAGAGGTTATCTGTGTGAGCTGCCCCG 238
|||||
34 IyGlnGlyProAlaAlaAspProLeuHISGlnAlaMetArgAlaIaGly 50
|||||
239 GGGAGGGCCGACGACCTGACCCGCTGCACCAAGCATGCGGCGACCTGA 288
|||||
51 AspGluPheGluThrArgPheArgThrPheSerAspLeuAlaIaGlu 67
|||||
289 GATGACTTGAAGACCCGCTTCCGGCCACCTTCTGTGATCGCGCGTCA 338
|||||
67 IleuHisValIThrProGlySerAlaGlnArgPheThrGlnValSer 84
|||||
339 GCTGATGTGACCCGAGCTCAGCCACCAAGCGTTCCACCGAGTCTCCG 388
|||||
84 sPglIleuPheGlnGlyProAspThrPglIaGlnValAlaPhePhe 100
|||||
389 ATGACATTTTCAAGGGGGCCCACTGCGGCGCTTGTAGCTCTCTTT 438
|||||

```

101 ValPheGlyValAlaLeuGlySerValaGlnSerValaGln 112  
|||||  
439 GTCTTTGGGCTCGACTGTGTGCTGAAGTGTTC 474

seq\_name: gb\_est2:BM191403

seq\_documentation\_block:

LOCUS BM191403 601 bp mRNA linear EST 11-DEC-2001  
DEFINITION d3186a10.y1 NICHD XGC L11 Xenopus laevis cDNA clone IMAGE:5129754  
5' similar to SW:ARL\_XENLA 091827 APOPTOSIS REGULATOR R1 ;, mRNA  
Sequence.  
ACCESSION BM191403  
VERSION BM191403.1 GI:17527366  
KEYWORDS EST.  
SOURCE African clawed frog.  
ORGANISM Xenopus laevis

## REFERENCE

1 (bases 1 to 601)  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Martha Redbert, Steven L. Klein, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: Xenopus clones from this library are available  
through the I.M.A.G.E. Consortium/LNL at: info@image.llnl.gov  
Seq primer: 40RP from Glibco  
High quality sequence stop: 386.

## FEATURES

## Source

Location/Qualifiers  
1..601  
/organism="Xenopus laevis"  
/db\_xref="taxon:8355"  
/clone="IMAGE:5129754"  
/clone\_1lb="NICHD XGC L11"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: liver; Vector: PCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.4 kb. Constructed by Life  
Technologies. Note: This is a Xenopus Gene Collection (XGC  
) library."  
BASE COUNT 149 a 125 c 189 g 138 t  
ORIGIN

## alignment\_scores:

Quality: 571.50 Length: 164  
Ratio: 4.112 Gaps: 1  
Percent Similarity: 84.756 Percent Identity: 66.463  
alignment\_block:  
US-09-155-327e-7 x BM191403 ..

Align seg 1/1 to: BM191403 from: 1 to: 601

```

11 ArgAlaLeuValAlaAspPheValGlyTyrIysLeuArgGlnGlyTyr 27
|||||
119 CGGGCTTTGGTGAGAGATTGTCGTCGACAGTTATGACCAACTACTCT 168
|||||
27 rValCysGlyIaGlyProGlyGlnGlyProAlaAlaAspProLeuHISG 44
|||||
169 TGT.....CCAGAGCTGACGAGACGACGATCTCTGCTTGCATT 209
|||||
44 IAlaMetArgAlaIaGlyAspGluPheGluThrArgPheArgThr 60
|||||
210 CAGCTATGCTGCTGACGAGGATGAATTGAGAGCGATTCAAGCAAGCA 259
|||||

```











OM of: US-09-155-327E-7 to: N\_Geneseq\_032802:\* out\_format: xls  
Date: Jun 6, 2002 2:37 PM

```

|||||
1 ATGGCGACCCAGCCCTCGGCCGACACAGAGGGCTCTGGTGGACACTT 50
17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
51 TGTAGGTTATTAAGCTGAGCGAAGGGGTATGTCTGTGAGCTGGCCCG 100
34 1ygluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
101 GGGAGGGCCCGACGACCTGACCCGCTGACCAACCATGGCGGACGCTGGA 150
51 AspGluPheGluThrArgPheArgArgTyrPheSerAspLeuAlaAlaG 67
151 GATGAGTTCGAGACCCGCTTCGCGCCACCTCTCTGATCTGGCGGCTCA 200
67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
201 GCGCATGTGACCCCGACGCTCAGCCCAACACAGCTTCACCCAGGTCTCG 250
84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
251 ATGAACTTTTTCAAAGGGGGCCCAACTGGGGCGGCTTGTACCTTCTTT 300
101 ValPheGlyAlaAlaLeuGlyAlaGlySerValAsnLysGluMetGluPr 117
301 GCTTTGGGGGCTGCACTGTGTCTGAGAGTGTCAACAAAGAGATGGAACC 350
117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
351 ACTGGTGGGACAAAGTGCAGAGAGTGGATGGCTTACCTGGAGAGCCGCC 400
134 euAlaAspTrpIleHisSerSerGlyGlyTTPAlaGluPheThrAlaLeu 150
401 TGGCTGACTGAGTCCACAGCACTGGGGCTGGCGGAGTTCACAGCTCTTA 450
151 TyrGlyAspGlyAlaLeuGlnGluAlaArgArgLeuArgGlnGlyAsnTr 167
451 TACGGGAGCGGGGCTTGGAGAGGCGCGGCTCTGCGGGAGGGAGACTG 500
167 PalAserValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
501 GGCATCACTGAGAGACAGTGTGACGGGGCGGCTGGCAGCTGGGGCCCTGG 550
184 alThrValGlyAlaPhePheAlaSerLys 193
551 TAACGTAGGGGCTTTTTCGTACCAAG 579
seq_name: /STD1/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:AAV28334
seq_documentation_block:
ID AAV28334 standard; cDNA; 579 BP.
XX
AC AAV28334;
XX
DT 02-OCT-1998 (first entry)
XX
DE Human bcl-2 gene.
XX
KW ss; bcl-2; cell death pathway; apoptotic; apoptosis; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..579
FT FT /*tag= a
FT FT /product= bcl-2
FT FT /note= "No stop codon given"
XX
PN US5789201-A.
XX
PD 04-AUG-1998.
XX
PF 11-FEB-1997; 97US-0798897.

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XX
PR 23-FEB-1996; 96US-0012201.
PR 11-FEB-1997; 97US-0798897.
XX
XX
PA (COCE-) COCENSYS INC.
XX
PI Guastella J;
XX
XX
DR WPI: 1998-446079/38.
DR P-PSDB; AAM61392.
XX
XX
PT Nucleic acids encoding B-cell lymphoma-2 protein - useful for
PT producing recombinant protein for use in treating uncontrolled cell
PT growth e.g. cancers
XX
XX
Claim 3; Column 15/16; 27pp; English.
XX
XX
CC The mammalian bcl-2 gene encode a protein that is a member of the bcl-2
CC family, components in the cell death pathway. The bcl-2 family
CC have both apoptotic activity and the apoptosis blocking activity. bcl-2
CC falls in the apoptosis activity category. The recombinant protein may
CC be used to prevent uncontrolled cell growth, either by its direct
CC administration to recombinant genetic constructs to increase its
CC expression in vivo. Also, antisense constructs can be used in disorders
CC where prevention of cell death is desired.
XX
XX
SO Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;

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alignment_scores:
  Quality: 1002.00      Length: 193
  Ratio: 5.219          Gaps: 0
  Percent Similarity: 99.482  Percent Identity: 99.482

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alignment\_block:

US-09-155-327E-7 x AAV28334 ..

Align seg 1/1 to: AAV28334 from: 1 to: 579

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1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspRh 17
1 ATGGCGACCCAGCCCTCGGCCGACACAGAGGGCTCTGGTGGAGACTT 50
17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
51 TGTAGGTTATTAAGCTGAGCGAAGGGGTATGTCTGTGAGCTGGCCCG 100
34 1ygluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
101 GGGAGGGCCCGACGACCTGACCCACATGCAACAGCTTGGCGGACGCTGGA 150
51 AspGluPheGluThrArgPheArgArgTyrPheSerAspLeuAlaAlaG 67
151 GATGAGTTCGAGACCCGCTTCGCGCCACCTCTCTGATCTGGCGGCTCA 200
67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
201 GCTGATGTGACCCCGAGGCTCAGCCCAACACAGCTTCACCCAGGTCTCG 250
84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
251 ATGAACTTTTTCAAAGGGGGCCCAACTGGGGCGGCTTGTAGCCTTTCTT 300
101 ValPheGlyAlaAlaLeuGlyAlaGlySerValAsnLysGluMetGluPr 117
301 GCTTTGGGGGCTGCACTGTGTCTGAGAGTGTCAACAAAGAGATGGAACC 350
117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
351 ACTGGTGGGACAAAGTGCAGAGATGATGGCTGCTGAGTGCAGAGCGGCC 400
134 euAlaAspTrpIleHisSerSerGlyGlyTTPAlaGluPheThrAlaLeu 150

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401 TGGCTGACGTGATCCACACAGTGGGGCTGGCGGAGTTCCACAGCTCTA 450  
 151 TYRGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167  
 451 TACGGGAGCGGGCCCTGGAGAGAGCGGCGCTGCGGAGAGGAGACTG 500  
 167 PALaseValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184  
 501 GGCACTCAGTCAGACAGTCTGACGGGGCCCTGGCAGCTGGGGCCCTGG 550  
 184 aThrValGlyAlaPhePheAlaSerIys 193  
 551 TAACTGTAGGGGCGCTTTTGTCTAGCAAG 579  
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 seq\_documentation\_block:  
 ID AAK15946 standard; cDNA: 579 BP.  
 AC AAK15946;  
 XX 20-MAY-1999 (first entry)  
 DE cDNA encoding the human bcl-2 protein.  
 XX Rat bcl-2 protein; Rbcl-2: human bcl-2 protein; Hbcl-2: bcl-2 homologue;  
 XX programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
 XX head trauma; Alzheimer's Disease; neural; muscular degenerative disease;  
 XX multiple sclerosis; myocardial infarction; vitally induced cell death;  
 XX aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
 XX premature cell death; cell death stimulator; prolonged cell life span;  
 XX Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;  
 XX parasite; ss.  
 XX Homo sapiens.  
 OS US5883229-A.  
 XX 16-MAR-1999.  
 PD 25-NOV-1997; 97US-0978523.  
 XX 23-FEB-1996; 96US-0012201.  
 XX 11-FEB-1997; 97US-0798897.  
 PR 25-NOV-1997; 97US-0978523.  
 XX (COCE-) COCENSYS INC.  
 PA Guastella J;  
 PI WPI; 1999-214150/18.  
 DR P-PSDB: AAW97392.  
 XX Novel bcl-2 homologues of the rat and human bcl-2 protein - useful  
 PT for modulating programmed cell death  
 PS Disclosure; Columns 15-16; 26pp; English.  
 XX The present sequence encodes human bcl-2 protein (Hbcl-2). The  
 CC specification also describes rat bcl-2 protein (Rbcl-2). Rbcl-2 and  
 CC Hbcl-2 are homologues of the bcl-2 protein thought to be involved in  
 CC programmed cell death (apoptosis and necrosis). Rbcl-2 and Hbcl-2  
 CC proteins may be used to treat conditions associated with a disruption of  
 CC the cell death pathway. If they act as cell death inhibitors, they may be  
 CC used in therapies to treat subjects suffering from: strokes, head trauma,  
 CC Alzheimer's Disease, neural and muscular degenerative diseases  
 CC (especially multiple sclerosis), myocardial infarction, vitally induced  
 CC cell death, aging, spinal cord injuries and amyotrophic lateral  
 CC sclerosis-conditions where cells under go premature cell death as a  
 CC result of triggers which may or may not be apparent. They may also be  
 CC used in this way to develop cell lines which remain viable in culture for  
 CC an extended period. In contrast, if they act as cell death stimulators,  
 CC Rbcl-2 and Hbcl-2 may be used to treat conditions associated with

CC prolonged cell life span such as cancer (especially Kaposi's sarcoma and  
 CC lung cancer) and auto/hyperimmune diseases. They may also be used to  
 CC cause cell death in, and hence control, parasites.  
 XX  
 XX Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;

alignment\_scores:  
 Quality: 1002.00 Length: 193  
 Ratio: 5.219 Gaps: 0  
 Percent Similarity: 99.482 Percent Identity: 99.482

alignment\_block:  
 US-09-155-327E-7 x AAK15946

Align seg 1/1 to: AAK15946 from: 1 to: 579

1 MetaIaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspH 17  
 1 AVGGCGACCCAGCCCTCGCCCGACACAGCGGCTCTGTGGAGACACTT 50  
 17 eValGlyThrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34  
 51 TGTAGTTATTAAGCTGAAGCAGAAAGGTTATCTGTGAGAGTGGCCCG 100  
 34 IyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50  
 101 GGGAGGCGCCACAGCTGACCTGACACCAAGCCATGCGGGAGCTGGA 150  
 51 AspGluPheGluThrArgPheArgThrPheSerAspLeuAlaIaGl 67  
 151 GATGACTTGACACCCCGCTCGGGGACCTTCCTGATCTGCGGGCCCA 200  
 67 nLeuHisValThrProGlySerAlaGlnArgPheThrGlnValSera 84  
 201 GCTGCACTGACCCCGCCAGCTCAGCCCAACACAGCTTACCCAGGCTCG 250  
 84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhe 100  
 251 ATGAACCTTTTCAAGGGGCGCCCACTGGGGCGCTTGTACCTTTT 300  
 101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluP 117  
 301 GCTTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 350  
 117 GluValGlyGluValGlnGlnLysPheValAlaTyrLeuGluThrArgL 134  
 351 ACTGTGGGACAGTGCAGAGAGTGGATGGGCTTACCTGAGACCGCGC 400  
 134 eAlaAspTrpIleHisSerSerGlyTyrTrpIaGluPheThrAlaLeu 150  
 401 TGGCTGACTGATCCACAGCAGTGGGGCTGGGGGAGTTCACAGCTCTA 450  
 151 TYRGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167  
 451 TACGGGAGCGGGCCCTGGAGAGAGCGGCGCTGCGGAGAGGAGACTG 500  
 167 PALaseValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184  
 501 GGCACTCAGTCAGACAGTCTGACGGGGCCCTGGCAGCTGGGGCCCTGG 550  
 184 aThrValGlyAlaPhePheAlaSerIys 193  
 551 TAACTGTAGGGGCGCTTTTGTCTAGCAAG 579  
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 seq\_documentation\_block:  
 ID AAK25133 standard; DNA: 581 BP.  
 AC AAK25133;  
 XX 05-JUL-1999 (first entry)  
 DT

XX Mouse bcl-w gene.

DE Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;

XX animal model; ss.

XX Mus sp.

XX WO9913710-A1.

XX 25-MAR-1999.

XX 16-SEP-1998; 98WO-AU00764.

XX 16-SEP-1997; 97AU-0009228.

XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

XX Adams J, Cory S, Gibson L, Koentgen F, Print C;

XX WPI: 1999-243890/20.

XX P-PSDB: AAY05531.

XX Claim 3; Page 34; 52pp; English.

The present sequence is the mouse bcl-w gene encoding Bcl-w protein (see AAY05531), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation in at least one allele of the human or murine bcl-w gene or in a gene associated with bcl-w. Such animals have disorganized seminiferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility.

Sequence 581 BP; 106 A; 158 C; 200 G; 117 T; 0 other;

alignment\_scores:

Quality: 1000.00 Length: 193  
Ratio: 5.181 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 98.964

alignment\_block:

US-09-155-327E-7 x AAX25133 ..

Align seg 1/1 to: AAX25133 from: 1 to: 581

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17 eValGlyTyrLysLeuArgLysGlyTyrValGlyGlyAlaGlyProG 34
51 TGTAGGCTATTAAGCTGAGGAGGAGGTATGTCTGTGGAGCTGGCCCTG 100
34 lYGIuGlyProAlaAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
101 GGGAGGCGCCAGCGCCGACCCCTGACCAACCATGGGGCTGCTGTA 150
51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaG 67
151 GACGAGTTGAGACCCGCTTCCGCGCACCTTCCTGACCTGGCCGCTCA 200

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67 nLeuHisValThrProGlySerAlaGlnGlnAlaArgPheThrGlnValSerA 84
201 GCTACAGCTGACCCAGGCTCAGCCAGCCAGACGCTTACACCGGTTTCCG 250
84 spGluLeuPheGlnGlyLysProAspThrGlyArgLeuValAlaPhePhe 100
251 ACGACTTTTCCAGAGGGGCCCTTAAGTGGGCGGCTGTGTGTCATTTCTT 300
101 ValPheGlyAlaAlaLeuCysAlaGluSerValaLeuLysGluMetGluPr 117
301 GTCTTTGGGGCTGCTGCTGTCTGAGAGTGCACAAAGAAATGGAGCC 350
117 oLeuValGlyGlnValGlnGluThrPheValAlaTyrLeuGluThrArgL 134
351 TTTGGTGGGACAAAGTCCAGAGATGTGATGTGCTTACCTGAGACAGCTC 400
134 eValAspTrpIleHisSerSerGlyTyrPalaGluPheThrAlaLeu 150
401 TGGCTGACTGGATCCACAGAGTGGGGCTGGGCGAGTTCACAGCTCTA 450
151 TyrGlyAspGlyAlaLeuGluGlnAlaAlaArgArgLeuArgLysAsnTr 167
451 TACGGGAGCGGGGCCCTGAGAGGACAGCGCTGCGGAGGGAACCTG 500
167 PalaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeu 184
501 GGCACTCACTGAGACAGTGTGACCGGGCGCGTGGCACTGGGGCCCTGG 550
184 AlThrValGlyAlaPhePheAlaSerLys 193
551 TAACTGTAGGGGCTTTTGTCTAGCAAG 579

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seq_documentation_block:
ID AAT96577 standard; DNA; 583 BP.
XX
XX AAT96577;
AC
XX
XX 22-APR-1998 (first entry)
DE
XX
XX Human bcl-w DNA.
KW
XX Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
XX diagnosis; degenerative disease; ss.
OS
XX Homo sapiens.
FH
XX Key Location/Qualifiers
FT CDS 1..582 /*tag= a
FT /product= bcl-w
XX
XX WO9735971-A1.
XX
XX 02-OCT-1997.
XX
XX 27-MAR-1997; 97WO-AU00199.
XX
XX 27-MAR-1996; 96AU-0008965.
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Adams JM, Cory S, Gibson LM, Holmgren SP;
XX WPI: 1997-489635/45.
XX P-PSDB: AAM36047.
XX
XX Nucleic acid encoding apoptosis related gene bcl-w - used to induce
XX or inhibit cell survival, e.g. for treatment of cancer and
XX degenerative diseases
XX

```



PS Claim 3: Page 48; 86pp; English.

CC This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene  
 CC family, extracted from an adult brain library. This gene promotes cell  
 CC survival, so its modulation is useful in treatment of cancer or  
 CC auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's  
 CC disease, myocardial infarct, muscular degeneration, hypoxia, ischemia,  
 CC human immunodeficiency virus infection or in cell transplants.  
 CC up-regulation of the gene can also be used to modify cell lines cultured  
 CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas  
 CC and to increase survival of primary explants during genetic modification.  
 CC It can be used to produce recombinant bcl-w for therapy, diagnosis,  
 CC antibody production or screening of potential modulators.

CC  
 CC  
 CC Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other:

alignment\_scores: Length: 193  
 Quality: 1000.00 Gaps: 0  
 Ratio: 5.181  
 Percent Similarity: 100.000 Percent Identity: 98.964

alignment\_block:  
 US-09-155-327e-7 x AAT96577 ..

Align seg 1/1 to: AAT96577 from: 1 to: 583

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 1 ATGGCGACCCAGCCTCGGCCACACAGCGGCTCTGGTGGCAGACTT 50  
 17 eValaGlyTrpLeuArgGlnLysGlyTrpValCysGlyAlaGlyProG 34  
 1 TGTAGCTTTAAGCTGAGCGACAGAGGTTATGTGTGAGCTGCCCCG 100  
 34 LysGlyLysProAlaAlaAspProLeuHisGlnAlaMetArgAlaAla 50  
 101 GGGAGAGGCCAGAGCTGACCGCTGACCCAGCCATCGGGCAGCTGA 150  
 51 AspGluPheGluThrArgPheArgThrPheSerAspLeuAlaAla 67  
 151 GATGAGTTCAGACCCGCTTCCGGCCACCTTCTGATCTGGCGCTCA 200  
 67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSer 84  
 201 GCTGCATGTGACCCAGGCTCAGCCAGCAAGCTTACCCAGGCTCCG 250  
 84 spGluLeuPheGlnGlyLysProAsnTrpGlyArgLeuValAlaPhe 100  
 251 ACGAACTTTTCAAGGGGCCCACTGGGGCCGCTTGTAGCTTCTTT 300  
 101 ValPheGlyAlaAlaLeuCysAlaGlnSerValAsnLysGlnMetGlu 117  
 301 CTCTTTGGGGCTGCATGTGTGTGAGAGTGTCAACAAGAGATGGAACC 350  
 117 cLeuValGlyGlnValGlnGlnLysTrpMetValAlaTrpLeuGluThrArg 134  
 351 ACTGTGGAGCAAGTCCAGAGTGGATGGTGGCTTACTGAGACGGGC 400  
 134 euAlaAspTrpIleHisSerSerGlyLysTrpAlaGlnPheThrAlaLeu 150  
 401 TGGTCGACTGATCCACAGCAGTGGGGCTGGGGAGTTTACAGCTCTA 450  
 151 TrpGlyAspGlyAlaLeuGlnGlnAlaArgArgLeuArgGlnGlyAsnTr 167  
 451 TACGGGGAGCGGGCCCTGGAGAGCGCGGCTGCGCGAGGAGACTG 500  
 167 palAserValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeu 184  
 501 GGCATATGATGAGGACAGTGTGACGGGGCCGTGGCTGGGGGGCCCTGG 550  
 184 alThrValGlyAlaPhePheAlaSerLys 193

551 TAACTGTAGGGCGCTTTTGTCTAGCAAG 579

seq\_name: /SIDS1/gcdata/geneseq/geneseq-emb1/NA199. DAT: AAX25134

seq\_documentation\_block:  
 ID AAX25134 standard; DNA: 583 BP.

AC AAX25134:  
 DT 05-JUL-1999 (first entry)

DE Human bcl-w gene derivative.

XX Spermatoogenesis; bcl-3 gene; bcl-2; human; fertility; infertility;

KW animal model; ss.

OS Homo sapiens.

PN WO9913710-A1.

PD 25-MAR-1999.

XX 16-SEP-1998; 98WC-AU00764.

PR 16-SEP-1997; 97AU-0009228.

PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

XX Adams J, Cory S, Gidson L, Koentgen F, Print C;

XX WPI: 1999-243890/20.

DR P-PSDB; AAY05532.

PT An animal model exhibiting reduced levels of a bcl-w protein and/or

PS protein associated with bcl-w

XX Disclosure; Page 36; 52pp; English.

XX The present sequence is described as a derivative of the human  
 CC bcl-w gene (see AAX25132) and encodes bcl-w protein (see AAY05532), a  
 CC pro-survival member of the bcl-2 family which is widely expressed  
 CC and which is essential for spermatogenesis. The invention relates  
 CC generally to a method of treatment and to an animal model for the  
 CC identification of molecules and genetic sequences useful for  
 CC inducing or reducing fertility of male animals. Methods are  
 CC provided for the treatment of infertility, or for reducing  
 CC fertility, by modulating spermatogenesis. An animal model carries  
 CC a mutation is at least one allele of the human or murine bcl-w gene  
 CC or in a gene associated with bcl-w. Such animals have disorganised  
 CC seminiferous tubules and are substantially infertile, but possess no  
 CC other major abnormalities as determined by histological examination.  
 CC They can be used to screen for therapeutic molecules including  
 CC genetic sequences capable of inducing, enhancing or otherwise  
 CC facilitating spermatogenesis in animals, or which can induce  
 CC infertility.

XX Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other:

alignment\_scores: Length: 193  
 Quality: 1000.00 Gaps: 0  
 Ratio: 5.181  
 Percent Similarity: 100.000 Percent Identity: 98.964

Percent Similarity: 100.000 Percent Identity: 98.964

alignment\_block:  
 US-09-155-327e-7 x AAX25134 ..

Align seg 1/1 to: AAX25134 from: 1 to: 583

1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAsp 17  
 1 ATGGCGACCCAGCCTCGGCCACACAGCGGCTCTGGTGGCAGACTT 50

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17 eValGIYrLYsLeuArGInLYsGIYrValLYsGIYrAlaGIYrProG 34
   |||||
51 TGTAAGTTATTAAGTGAAGCAGAAAGGTTATGTCTGTGAGCTGGCCCG 100
   |||||
34 LYGIUGLYProAlaAlaAspProLeuHisGlnAlaMetArGAlaIaGIY 50
   |||||
101 GGGAGGGCCAGCAGCTGACCCCTCCACCAAGCCATGGGGGAGCTGTA 150
   |||||
51 AspGluPheGluThrArGArGArGThrPheSerAspLeuAlaAlaGI 67
   |||||
151 GATGAGTTCAGACGCCGCTTCGCCGCTTCTGTGATGGCGGCTCA 200
   |||||
67 nLeuHisValThrProGlySerAlaGlnGlnArGpPheThrGlnValSera 84
   |||||
201 GCTGCAATGTGACCCCGCTCAGCCAGCAAGCCTTCAACCCAGGTCTCCG 250
   |||||
84 sPGLuLeuPheGlnGlnLYrProAsnTrPGLYArGLeuValAlaPhePhe 100
   |||||
251 ACGAACTTTTTCAGGGGGCCCAACTGGGGCGCTTGTAGCCCTTCTTT 300
   |||||
101 ValPheGlyAlaAlaLeuCysAlaGlnSerValAsnLYsGlnMetGluPr 117
   |||||
301 CTCCTTGGGGCTGCACTGTGTCTGAGAGTGTCAACAAGAGATGGAACC 350
   |||||
117 oLeuValGlnGlnValGlnGlnUTrPMeTValAlaTYrLeuGlnUTrArGL 134
   |||||
351 ACTGGTGGACAAAGTCAGAGATGTGATGTGCTTACCTGGAGACGCCGC 400
   |||||
134 eUAlaAspTrPLeuHisSerSerGlyTYrTPAlaGluPheThrAlaLeu 150
   |||||
401 TGGTGCAGTGTGATCCACAGCAGTGGGGGCTGGGGAGTTCCACAGCTTA 450
   |||||
151 TYrGIYAspGLYAlaLeuGlnGlnAlaArGArGLeuArGlnLYsAnTr 167
   |||||
451 TAGGGGAGCGGGGCCCTGGAGAGCGCGCTGCGGAGGGAACCTG 500
   |||||
167 pAlaSerValArGThrValLeuThrGlyAlaValAlaLeuGlyAlaLeu 184
   |||||
501 GGCATCAGTGTAGACAGTGTGACGAGGGGCGCTGGGACTGGGGCCCTG 550
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184 aLTPrValGlyAlaPhePheAlaSerLYs 193
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551 TAAGTGTAGGGGCTTTTGTGTAGCAAG 579
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seq_documentation block:
ID AAV28333 standard: CDNA, 579 BP.
AC AAV28333;
XX
DT 02-OCT-1998 (first entry)
DE
XX
XX Rat bcl-y gene.
XX
XX ss: bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
OS
XX
XX Rattus sp.
XX
XX Key Location/Qualifiers
XX CDS 1..579
XX FT /*tag= a
XX FT /product= bcl-y
XX FT /note= "No stop codon given"
XX
XX US5789201-A.
XX
XX PD 04-AUG-1998.
XX
XX PF 11-FEB-1997; 97US-0798897.
XX
XX PR 23-FEB-1996; 96US-0012201.
XX PR 11-FEB-1997; 97US-0798897.

```

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XX
XX (CODE-) COGENS INC.
XX
XX Guastella J;
XX
XX WPI: 1998-446079/38.
XX P-PSDB: AAM61391.
XX
XX Nucleic acids encoding B-cell lymphoma-y protein - useful for
XX producing recombinant protein for use in treating uncontrolled cell
XX growth e.g. cancers
XX
XX Claim 2: Column 13/14; 27pp; English.
XX
XX The mammalian bcl-y genes encode a protein that is a member of the bcl-2
XX family, components in the cell death pathway. The bcl-2 family
XX have both apoptotic activity and the apoptosis blocking activity. bcl-y
XX falls in the apoptosis activity category. The recombinant protein may
XX be used to prevent uncontrolled cell growth, either by its direct
XX administration to recombinant genetic constructs to increase its
XX expression in vivo. Also, antisense constructs can be used in disorders
XX where prevention of cell death is desired.
XX
XX Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 other;
XX
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XX alignment_scores:
XX Quality: 996.00 Length: 193
XX Ratio: 5.161 Gaps: 0
XX Percent Similarity: 100.000 Percent Identity: 98.446
XX
XX alignment block:
XX US-09-155-327e-7 x AAV28333
XX
XX Align seg 1/1 to: AAV28333 from: 1 to: 579
XX
XX 1 MetaLathrProAlaSerAlaProAspThrArGAlaLeuValAlaAspH 17
XX |||||
XX 1 ATGGCGACCCCGAGCTTCAACCCAGACACAGGGCTGTAGTGGCTGACT 50
XX |||||
XX 51 TGTAAGCTATTAAGCTGACAGAAAGGTTATGTCTGTGAGCTGGCCCTG 100
XX |||||
XX 34 LYGIUGLYProAlaAlaAspProLeuHisGlnAlaMetArGAlaIaGIY 50
XX |||||
XX 101 GGGAGGGCCAGCAGCCGCGCTGACCAAGCCATCGGGGAGCTGGA 150
XX |||||
XX 51 AspGluPheGluThrArGArGArGThrPheSerAspLeuAlaAlaGI 67
XX |||||
XX 151 GACGAGTTTGAGACCCCGCTTCCGGGCACTTCTGTGACTGGCCGCTCA 200
XX |||||
XX 67 nLeuHisValThrProGlySerAlaGlnGlnArGpPheThrGlnValSera 84
XX |||||
XX 201 GCTACAGTGTGACCCAGGCTCAGCCAGCAAGCCTTCAACCCAGGTTCG 250
XX |||||
XX 84 sPGLuLeuPheGlnGlnLYrProAsnTrPGLYArGLeuValAlaPhePhe 100
XX |||||
XX 251 ACGAACTTTTTCAGGGGGCCCAACTGGGGCGCTTGTGAGCTTCTTT 300
XX |||||
XX 101 ValPheGlyAlaAlaLeuCysAlaGlnSerValAsnLYsGlnMetGluPr 117
XX |||||
XX 301 CTCCTTGGGGCTGCACTGTGTCTGAGAGTGTCAACAAGATGGAAGCC 350
XX |||||
XX 117 oLeuValGlnGlnValGlnGlnUTrPMeTValAlaTYrLeuGlnUTrArGL 134
XX |||||
XX 351 ATTGGTGGACAAAGTGCAGATGTGATGTGACTTACCTGAGACACGCT 400
XX |||||
XX 134 eUAlaAspTrPLeuHisSerSerGlyTYrTPAlaGluPheThrAlaLeu 150
XX |||||
XX 401 TGGCTGAGTGTGATCCACAGCAGTGGGGGCTGGGGAGTTCCACAGCTTA 450
XX |||||
XX 151 TYrGIYAspGLYAlaLeuGlnGlnAlaArGArGLeuArGlnLYsAnTr 167

```

```

|||||
451 TACGGGAGCGGCCCTGGAGAGGACGGGCTCTCCGGAGGGAACTG 500
167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
|||||
501 GGCACTACGTAGAGACAGTCTGACGGGGCTGTGGCACTGGGGCCCTGG 550
184 aThrValGlyAlaPhePheAlaSerLys 193
|||||
551 TAACTGTAGGGGCTTTTGTGCTAGCAAG 579
seq_name: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AA15945

```

```

seq_documentation_block:
ID   AAX15945 standard; cDNA, 579 BP.
XX
XX   AAX15945;
AC   20-MAY-1999 (first entry)
DE   cDNA encoding the rat bcl-2 protein.
XX
XX   Rat bcl-2 protein; Rbcl-2; human bcl-2 protein; Hbcl-2; bcl-2 homologue;
KM   programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KM   head trauma; Alzheimer's disease; neural; muscular degenerative disease;
KM   multiple sclerosis; myocardial infarction; vitally induced cell death;
KM   aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KM   premature cell death; cell death stimulator; prolonged cell life span;
KM   Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
KM   parasite; ss.
XX
XX   Rattus sp.
OS   US5883229-A.
XX
XX   16-MAR-1999.
PD   25-NOV-1997; 9705-0978523.
XX
XX   23-FEB-1996; 9605-0012201.
XX
XX   11-FEB-1997; 9705-0798897.
PR   25-NOV-1997; 9705-0978523.
XX
XX   (COCE-) COCENSYS INC.
PA   Guastella J;
PI   MPI: 1999-214150/18.
XX
XX   P-PSDB; AAM97391.
DR   Novel bcl-2 homologues of the rat and human bcl-2 protein - useful
PT   for modulating programmed cell death
XX
XX   disclosure; Columns 13-16; 26pp; English.
PS   The present sequence encodes rat bcl-2 protein (Rbcl-2). The
XX   specification also describes human bcl-2 protein (Hbcl-2). Rbcl-2 and
CC   Hbcl-2 are homologues of the bcl-2 protein thought to be involved in
CC   programmed cell death (apoptosis and necrosis). Rbcl-2 and Hbcl-2
CC   proteins may be used to treat conditions associated with a disruption of
CC   the cell death pathway. If they act as cell death inhibitors, they may be
CC   used in therapies to treat subjects suffering from: strokes, head trauma,
CC   Alzheimer's disease, neural and muscular degenerative diseases
CC   (especially multiple sclerosis), myocardial infarction, vitally induced
CC   cell death, aging, spinal cord injuries and amyotrophic lateral
CC   sclerosis conditions which may or may not be apparent. They may also be
CC   result of triggers which may or may not be apparent. They may also be
CC   used in this way to develop cell lines which remain viable in culture for
CC   an extended period. In contrast, if they act as cell death stimulators,
CC   Rbcl-2 and Hbcl-2 may be used to treat conditions associated with
CC   prolonged cell life span such as cancer (especially Kaposi's sarcoma and
CC   lung cancer) and autoimmune diseases. They may also be used to
CC   cause cell death in, and hence control, parasites.

```

```

XX
SQ   Sequence 579 BP: 111 A; 157 C; 198 G; 113 T; 0 other;
alignment_scores:
    Quality: 996.00      Length: 193
    Ratio: 5.161        Gaps: 0
Percent Similarity: 100.000    Percent Identity: 98.446
alignment_block:
US-09-155-327e-7 x AAX15945 ..
Align seg 1/1 to: AAX15945 from: 1 to: 579

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```

1 MetAlaThrProAlaSerAlaProAspThrArgAlaAlaLeuValAlaAspPh 17
|||||
1 ATGGCGACCCCGACCTCAACCCAGACACAGCGGGCTCTAGTGGCTGACTT 50
17 eValGlyTrpLysLeuArgGlnLysGlyTrpValCysGlyAlaGlyProG 34
|||||
51 TGTAGGCTATAGCTGAGACAGAGGTTATGTCCTGGAGCTGGCCCTG 100
34 LyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
|||||
101 GGAGAGGCCAGCAGCCGACCCGCTGCACCAACCAATGGCGCAGCTGGA 150
101 GGAGAGGCCAGCAGCCGACCCGCTGCACCAACCAATGGCGCAGCTGGA 150
51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaG 67
151 GACGAGTTTGAGACCCGCTTCGGCGCACCTTCTGACCTGGCCGCTCA 200
67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
|||||
201 GCTACAGCTGACCCAGGCTCAGCCAGCAACGCTTACCAGGTTCCG 250
84 SPGLnLeuPheGlnGlnLysLysProAsnTrpGlyArgLeuValAlaPhePhe 100
|||||
251 ACGAAGCTTTCCAGGGGGCCCAACTGGGCGCGCTTGGCACTTCTT 300
101 ValPheGlyAlaAlaLeuCysAlaGlnSerValAsnLysGluMetGluPr 117
|||||
301 GTCTTTGGGCTGCCCTGTGTCTCAGAGTCAACAAAGAAATGAGACC 350
117 oLeuValGlyGlnValGlnGluTrpMetValAlaTrpLeuGluThrArgL 134
|||||
351 ATTGGTGGGACAAAGTCAGATGATGATGATGATGATGATGATGATGAT 400
134 euAlaAspTrpPheHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
|||||
401 TGGCTGACTGGATCCACAGCAGTGGGGCTGGCGGAGTTCACAGCTCTA 450
151 TyrGlyAspGlyAlaLeuGluGlnAlaArgArgLeuArgGluGlyAsnTr 167
|||||
451 TACGGGAGCGGCCCTGGAGAGGACGGGCTCTCCGGAGGGAACTG 500
167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
|||||
501 GGCACTACGTAGAGACAGTCTGACGGGGCTGTGGCACTGGGGCCCTGG 550
184 aThrValGlyAlaPhePheAlaSerLys 193
551 TAACTGTAGGGGCTTTTGTGCTAGCAAG 579
seq_name: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:AA196578
seq_documentation_block:
ID   AAT96578 standard; DNA; 581 BP.
XX
XX   AAT96578;
AC   22-APR-1998 (first entry)
DT   Mouse bcl-2 DNA.
XX

```

KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;  
 XX diagnosis; degenerative disease; ss.

OS Mus sp.

Key Location/Qualifiers  
 FT 1..507  
 FT /\*tag= a  
 FT /product= bcl-w  
 FT /note= "q"

W09735971-A1.

02-OCT-1997.

27-MAR-1997; 97WO-AU00199.

27-MAR-1996; 96AU-0008965.

(AMRA-) AMRAD OPERATIONS PTY LTD.

Adams JM, Cory S, Gibson LM, Holmgren SP;

WPI; 1997-489635/45.

P-PSDB; AAW36048.

PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce  
 PT or inhibit cell survival, e.g. for treatment of cancer and  
 PT degenerative diseases

PS Claim 3; Page 50-51; 86pp; English.

CC This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene  
 CC family. This gene promotes cell survival, so its modulation is useful in  
 CC treatment of cancer or auto-immune diseases, degenerative diseases (e.g.  
 CC stroke, Alzheimer's disease, myocardial infarct, muscular degeneration,  
 CC hypoxia, ischaemia, human immunodeficiency virus infection or in cell  
 CC transplants. Up-regulation of the gene can also be used to modify cell  
 CC lines cultured in vivo, e.g. to develop new lines, to facilitate  
 CC isolation of hybridomas and to increase survival of primary explants  
 CC during genetic modification. It can be used to produce recombinant Bcl-w  
 CC for therapy, diagnosis, antibody production or screening of potential  
 CC modulators.

SO Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 other;

alignment\_scores:

Quality: 965.00 Length: 193  
 Ratio: 5.079 Gaps: 0  
 Percent Similarity: 98.446 Percent Identity: 94.819

alignment\_block:

US-09-155-327E-7 x AAT96578

Align seg 1/1 to: AAT96578 from: 1 to: 581

1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17  
 1 ATGCGGACCCGACGCTCAACCCAGACACACGCGCTAGGCGGACTT 50  
 17 eValGlyTyrLeuArgGlnIleGlyTyrValCysGlyIleGlyProG 34  
 51 TGTAGGCTATAGGCTGAGGACAGAGGTTATGCTGTGAGACTGGGCTG 100  
 34 IyGIGlyProAlaAlaAspProLeuHisGlnAlaMetAlaGAlaGly 50  
 101 GGGAAAGCCGACCCGCGGCTGACCAAGCATGGCGGCTGCGGA 150  
 51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaGly 67  
 151 GACGAGTTGAGACCCGTTTCCGCGCACCTTCTGACCTGGCGGCTCA 200

67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSera 84  
 201 GCTACAGGTGACCCGACGCTCAACCCAGACACGCTTCAACGAGTTCCG 250

84 spGluLeuPheGlnGlyIleProAsnTrpGlyArgLeuValAlaPhePhe 100

251 ACGAAGTTTCCAAAGGGGCGCTTAAGTGGGCGCTTGTGGCATTCTTT 300

101 ValPheGlyValAlaLeuGlnCysAlaGlnSerValAsnLysGlnMetGluP 117

301 GTCTTTGGGGCTGCTGCTGTCTCTGAGAGTGTCAACAAGAAATGAGACC 350

117 oLeuValGlyIleValGlnGluTrpMetValAlaTyrLeuGlnThrArgL 134

351 TTTGGTGGGACAAATCCAGATTGATGATGCTGGCTGAGACAGCTC 400

134 eAlaAspTrpIleHisSerGlyIleTyrPAlaGluPheThrAlaLeu 150

401 TGGCTGACTGATCCACAGCAGTGGGCTGGCGGACTTCACAGCTCTA 450

151 TyrGlyAspGlyAlaLeuGlnGluAlaArgArgLeuArgGlnGlyAsnTr 167

451 TACGGGAGAGGGGCGCTGAGAGGACGACAGGCGCTGGGAGAGGCAACTG 500

167 PalAspValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184

501 GGCATGACTGAGACACAGTGTGACGGGCGCTGGCAGCTGGGCGCTCG 550

184 AlThrValGlyAlaPhePheAlaSerLys 193

551 TAAGTGTAGGGGCGCTTTTGTCTAGCAAG 579

seq\_name: /SDSL/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:AA25135

seq\_documentation\_block:

ID AAX25135 standard; DNA; 581 BP.

XX AAX25135;

AC 05-JUL-1999 (first entry)

DE Mouse bcl-w gene derivative.

KW Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;

XX animal model; ss.

OS Mus sp.

XX Key

XX CDS

XX W09913710-A1.

XX 25-MAR-1999.

XX 16-SEP-1998; 98WO-AU00764.

XX 16-SEP-1997; 97AU-0009228.

XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

XX Adams J, Cory S, Gibson L, Koentgen F, Print C;

XX WPI; 1999-243890/20.

XX P-PSDB; AAY05533.

XX An animal model exhibiting reduced levels of a Bcl-w protein and/or

XX protein associated with Bcl-w

XX Disclosure; Page 38; 52pp; English.

XX The present sequence is described as a derivative of the mouse

```

184  althrwalglYAlaIaphhepHealaserLys 193
      |||||||||||||||||||||||||
551  TAACTGTATGGGCCCTTTTCTTCAAG 579

seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV41925

seq_documentation_block:
ID  AAV41925 standard; cDNA; 1098 BP.
XX
XX  AAV41925;
AC
XX
XX  20-NOV-1998 (first entry)
DE
XX  Nucleotide sequence of the cDNA clone Bcl-1like (HAICH29).
DE
XX  Bcl-1like (HAICH29): chronic inflammatory disease; allergic reaction;
KM  Immunological disorder; autoimmune disease; anti-infectious agent; ss
XX
XX  -----

```

```

seq_name: /S1D1/gcgdata/geneseq/geneseqn-emb1/NM1998.DAT:AAV41925
seq_documentation_block:
ID   AAV41925 standard; cDNA; 1098 BP.
XX
XX
AC   AAV41925;
XX
XX
DI   20-NOV-1998 (first entry)
XX
XX
DE   Nucleotide sequence of the cDNA clone Bcl-1like (HAICH29).
XX
XX
KW   Bcl-1like (HAICH29); chronic inflammatory disease; allergic r
KW   immunological disorder; autoimmune disease; anti-infectious
XX
XX
OS   Homo sapiens.
XX
XX
Key      Location/Qualifiers
FH       1..1098
FT       CDS
FT       /*tag= a
FT       /product= "Bcl-1like (HAICH29) protein"
XX
XX
FN       WO9831800-A2.

```

product = "Bcl-1 like (HAICH29) protein"

W09831800-A2.

23-JUL-1998

21-JAN-1998; 98WO-US00960

21-JAN-1997; 97US-0034205

**Figure 1**

(HUMA-) HUMAN GENOME SCI INC.

Feng P, Gentz RL, Krissansen GW, Ni J, Rosen CA,

1  
1  
1  
1  
1

P-PsDB; AAW59884.

New isolated polynucleotides and encoded polypeptides - used to

infections, autoimmune diseases, allergies

TO CONTINUE

CLAIM 2, FIG 1A AND 1B) ABOVE: ---

This is the nucleotide sequence of the cDNA clone Bc1-1ike (Halc927). CC  
CC used in the method of the invention. The products of the clone can be CC  
CC used for treating conditions associated with abnormal expression of CC  
CC the polypeptides. They can be used for e.g. treating chronic CC  
CC inflammatory diseases, immunological disorders, autoimmune diseases, CC  
CC inflammatory diseases, various allergies, and as anti-infectious agents CC  
CC The products can also be used for detection and diagnosis.

Sequence 1098 BP; 264 A; 279 C; 325 G; 230 T; 0 other,

alignment_scores:	Length:	144
quality:	Gaps:	0
Ratio:	Percent Identity:	100.0000
Percent Similarity:		100.000

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alignment_block:
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Align seg 1/1 to: AAV41925 from: 1 to: 1098

1 MetaLaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17

```

|||||
1  ATGGGAGCCCGCCGCTCGCCCGCCAGACACAGGGCTCTGTGTCACACTT 50
17  eValGlYTrLysLeuArGlnLysGlyTrValLysGlyAlaGlyProG 34
51  TGTAGGTATTAAGCTGAGGCAAGAGGGTATGTTCTGTGAGCTGGCCCG 100
34  LylGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaGly 50
101  GGGAGGGCCCGAGCTGAGCCCGCTGCACCAACGATGGCGGAGCTGSA 150
51  AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAla 67
151  GATGAGTTCGAGACCCGCTTCGGCCGACCTCTCTGATCTGGCGGCTCA 200
67  nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSer 84
201  GGTGATGTGACCCCGAGGCTGACGCCCAACAAGACGCTTCACCCAGG 250
84  spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhe 100
251  ATTAACCTTTTCAAGGGGGCCCAACTGGGGCCCGCTGTACCTTCTTT 300
101  ValPheGlyAlaAlaLeuCysAlaGlnSerValaLysGluMetGluPr 117
301  GTCTTGGGGGCTGCACCTGTCTGTCTGAGAGTCAACAAGAGAGTGAAC 350
117  OleuValGlyGlnValGlnGluTrpMetValAlaTrpLeuGluThrArg 134
351  ACTGGGGGAGCAAGTCAGAGAGTGAATGATGATGGCTTACTGAGAGCG 400
134  eUAlaAspTrpIleHisSerSerGlyTrp 144
401  TGGCTGACTGATCCACAGCACTGGGGGCTGG 432

seq_name: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV59630
seq_documentation_block:
ID  AAV59630 standard; DNA; 1864 BP.
XX
AC  AAV59630;
XX
DT  19-JAN-1999 (first entry)
XX
DE  Human secreted protein gene 120 clone HGBZ64.
XX
KW  Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW  diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW  developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW  immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW  inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW  cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW  osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW  endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS  Homo sapiens.
XX
PN  WC9839448-A2.
XX
PD  11-SEP-1998.
XX
PF  06-MAR-1998; 98WO-US04493.
XX
PR  02-OCT-1997; 97US-0061060.
PR  07-MAR-1997; 97US-0038621.
PR  07-MAR-1997; 97US-0040161.
PR  07-MAR-1997; 97US-0040162.
PR  07-MAR-1997; 97US-0040163.
PR  07-MAR-1997; 97US-0040333.
PR  07-MAR-1997; 97US-0040334.
PR  07-MAR-1997; 97US-0040336.
PR  07-MAR-1997; 97US-0040626.
PR  11-APR-1997; 97US-0043311.

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PR  11-APR-1997; 97US-0043312.
PR  11-APR-1997; 97US-0043313.
PR  11-APR-1997; 97US-0043314.
PR  11-APR-1997; 97US-0043568.
PR  11-APR-1997; 97US-0043569.
PR  11-APR-1997; 97US-0043576.
PR  11-APR-1997; 97US-0043578.
PR  11-APR-1997; 97US-0043580.
PR  11-APR-1997; 97US-0043669.
PR  11-APR-1997; 97US-0043670.
PR  11-APR-1997; 97US-0043671.
PR  11-APR-1997; 97US-0043672.
PR  11-APR-1997; 97US-0043674.
PR  23-MAY-1997; 97US-0047492.
PR  23-MAY-1997; 97US-0047500.
PR  23-MAY-1997; 97US-0047501.
PR  23-MAY-1997; 97US-0047502.
PR  23-MAY-1997; 97US-0047503.
PR  23-MAY-1997; 97US-0047581.
PR  23-MAY-1997; 97US-0047582.
PR  23-MAY-1997; 97US-0047583.
PR  23-MAY-1997; 97US-0047584.
PR  23-MAY-1997; 97US-0047585.
PR  23-MAY-1997; 97US-0047586.
PR  23-MAY-1997; 97US-0047587.
PR  23-MAY-1997; 97US-0047588.
PR  23-MAY-1997; 97US-0047589.
PR  23-MAY-1997; 97US-0047590.
PR  23-MAY-1997; 97US-0047592.
PR  23-MAY-1997; 97US-0047593.
PR  23-MAY-1997; 97US-0047594.
PR  23-MAY-1997; 97US-0047595.
PR  23-MAY-1997; 97US-0047596.
PR  23-MAY-1997; 97US-0047597.
PR  23-MAY-1997; 97US-0047598.
PR  23-MAY-1997; 97US-0047599.
PR  23-MAY-1997; 97US-0047600.
PR  23-MAY-1997; 97US-0047601.
PR  23-MAY-1997; 97US-0047612.
PR  23-MAY-1997; 97US-0047613.
PR  23-MAY-1997; 97US-0047614.
PR  23-MAY-1997; 97US-0047615.
PR  23-MAY-1997; 97US-0047617.
PR  23-MAY-1997; 97US-0047618.
PR  23-MAY-1997; 97US-0047632.
PR  23-MAY-1997; 97US-0047633.
PR  06-JUN-1997; 97US-0048964.
PR  13-JUN-1997; 97US-0048974.
PR  08-JUL-1997; 97US-0049610.
PR  16-JUL-1997; 97US-0051926.
PR  18-AUG-1997; 97US-0052874.
PR  22-AUG-1997; 97US-0055724.
PR  22-AUG-1997; 97US-0056630.
PR  22-AUG-1997; 97US-0056631.
PR  22-AUG-1997; 97US-0056632.
PR  22-AUG-1997; 97US-0056636.
PR  22-AUG-1997; 97US-0056637.
PR  22-AUG-1997; 97US-0056662.
PR  22-AUG-1997; 97US-0056664.
PR  22-AUG-1997; 97US-0056845.
PR  22-AUG-1997; 97US-0056862.
PR  22-AUG-1997; 97US-0056864.
PR  22-AUG-1997; 97US-0056872.
PR  22-AUG-1997; 97US-0056874.
PR  22-AUG-1997; 97US-0056875.
PR  22-AUG-1997; 97US-0056876.
PR  22-AUG-1997; 97US-0056877.
PR  22-AUG-1997; 97US-0056878.
PR  22-AUG-1997; 97US-0056879.
PR  22-AUG-1997; 97US-0056880.
PR  22-AUG-1997; 97US-0056881.
PR  22-AUG-1997; 97US-0056882.
PR  22-AUG-1997; 97US-0056884.

```





CC leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel  
CC diseases. The present sequence is a gene of the invention.  
XX  
SQ Sequence 6049 BP; 1480 A; 109 C; 1549 G; 2911 T; 0 other;

alignment\_scores:  
Quality: 444.00 Length: 144  
Ratio: 3.795 Gaps: 0  
Percent Similarity: 81.250 Percent Identity: 65.278

alignment\_block:  
US-09-155-327e-7 x ABL32228 ..

Align seg 1/1 to: ABL32228 from: 1 to: 6049

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1 MetalThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspH 17
||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||
5001 ATGGCATTTTACTTTCGCTTTAGATATACGGCTTTGCTGCTGATTT 5050
17 eValGlyTyrLysLeuArgLysGlyValCysGlyAlaGlyProG 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
5051 TGAAGCTATATAGTTCAGTAGAGGCTATGTTGTGAGTTGCTTCG 5100
34 lYGLGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
5101 GGGAGGTTTATAGTTCGCTGATTAAGTATACGGGCTGCTGCTGGA 5150
51 AspGluPheGluThrArgPheArgThrPheSerAspLeuAlaAlaG 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
5151 GATGAGTTCGACATTCGCTTTGCGGCTATTTTTCGATTTCGCGTTTA 5200
67 nLeuHisValThrProGlySerAlaGlnLysArgPheThrGlnValSerA 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
5201 GTTGTATGCTGATTTTATGCTTATTAACGCTTATTAAGCTTCGCG 5250
84 sPGLnLeuPheGlnGlyLysProAsnTrpGlyArgLeuValAlaPhe 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
5251 ATGCAATTTTAAAGCGGCTTTAATTGGGCTTTGCTGCTGCTTTT 5300
101 ValPheGlyAlaAlaLeuCysAlaGlnSerValAsnLysGluMetGluPr 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
5301 GTTTTGGGCTGCTATGCTGCTGCTAGAGTGTATATAGAGATGCAAT 5350
117 OlenuValGlyLysValGlnGluTrpMetValAlaTyrLeuLysThrArgL 134
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
5351 ATGCTGCGGATTAAGTGTAGAGAGTGGCTGCTTATTTTGGAGACG 5400
134 euAlaAspTrpPLeuHisSerSerGlyGlyTrp 144
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
5401 TGGTGTATGCTTATTAAGTGTAGTGGGCTTCG 5432

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seq\_name: /SIDSL/gcgdata/geneseq/geneseg-emb1/NA2001A.DAT: AAS00247  
seq\_documentation\_block:  
ID AAS00247 standard; DNA; 1236 BP.

XX AAS00247;  
XX  
XX 31-MAY-2001 (first entry)  
XX  
XX Bcl-XL-DTR apoptosis-modifying fusion protein, DNA sequence.  
XX  
XX Human: Bcl-XL-DTR; apoptosis; cancer; spinal muscular atrophy; ds;  
XX diptheria toxin receptor binding domain; DTR; neoplasm; tumour;  
XX hyper-proliferation; Alzheimer's disease; neurodegenerative disorder;  
XX transient ischaemic neuronal injury; stroke; spinal cord injury;  
XX Huntington's disease.  
XX  
XX Chimeric - Homo sapiens.  
OS Chimeric - Corynebacterium diptheriae.  
OS Chimeric - Synthetic.

```

XX key Location/Qualifiers
FH CDS 1..1236
FT /*tag= a
FT /product= "Bcl-XL-DTR fusion protein"
FT /note= "DTR is diptheria toxin receptor binding domain"
FT 7..36
FT /*tag= b
FT /note= "10x Histidine tag"
FT 61..759
FT /*tag= c
FT /note= "Bcl-XL gene from codon 1-233"
FT 760..777
FT /*tag= d
FT /note= "linker DNA, linking Bcl-XL to DTR"
FT 778..1236
FT /*tag= e
FT /note= "DTR, diptheria toxin receptor binding domain"

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W0200112661-A2.

22-FEB-2001.

15-AUG-2000; 2000WO-US22293.

16-AUG-1999; 99US-0149220.

(HARD) HARVARD COLLEGE.  
(USSH) US DEPT HEALTH & HUMAN SERVICES.

Youle RJ, Liu X, Collier RJ;

WPI; 2001-218343/22.

P-PSDB; AAU00219.

Novel fusion protein for modifying apoptosis in target cell and  
reducing apoptosis after transient ischemic neuronal injury, has two  
domains which targets protein to a cell and modifies apoptotic response  
of cell  
Claim 5; Page 54-56; 65pp; English.

The sequence represents the coding sequence of Bcl-XL-DTR apoptosis-  
modifying fusion protein comprising human Bcl-XL sequence fused via a  
short linker to diptheria toxin receptor binding domain (DTR). The  
functional apoptosis-modifying fusion protein is capable of binding a  
target cell and integrating into or crossing a cellular membrane of the  
target cell. The apoptosis-modifying fusion protein comprises at least  
two domains: the DTR domain, which targets the fusion protein to the  
target cell and the Bcl-XL domain, which modifies an apoptotic response  
(inhibiting or enhancing) apoptosis in a target cell, for modifying  
lymphocyte, cancer, neoplasm, macrophage, epithelial, stem, tumour or  
hyper-proliferative cell or an adipocyte. It is also useful for reducing  
apoptosis in a subject after transient ischaemic neuronal injury,  
especially spinal cord injury. The fusion protein may be used to treat  
various diseases and injury conditions through inhibition or enhancement  
of apoptotic cellular response, including neurodegenerative disorders  
such as Alzheimer's disease, Huntington's disease, spinal muscular  
atrophy, stroke episodes and unregulated cell growth as in tumours and  
various cancers. The apoptosis-modifying fusion protein can be delivered  
effectively throughout the body and targeted to selective tissue and  
cells.

Sequence 1236 BP; 317 A; 291 C; 343 G; 285 T; 0 other;

alignment\_scores:  
Quality: 433.50 Length: 233  
Ratio: 2.949 Gaps: 4  
Percent Similarity: 63.090 Percent Identity: 39.914

alignment\_block:



US-09-155-327E-7 x AAS00247

Align seg 1/1 to: AAS00247 from: 1 to: 1236

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76 CGGAGAGTGTGGTGTGACTTCTCTCTACAAAGCTTTCACGAAAGGATA 125
27 I..... 27
126 CAGCTGAGTCAGTTAGTATGTGAAAGAACAGAGCTGAGGCCCGAC 175
   .....ValCysGlyAlaGlyPro 33
28 ..... 33
176 AAGGAGCTGATCGAGATGAGAGCCCGACGTGCATCAATGCAACCCCA 225
   .....GlyGluGlyProAlaAlaAsp..... 40
34 ..... 40
226 TCCTGGCAGCTGGCAGACAGCCCGCGGTGATGAGAGCCCTGCGCACAG 275
   .....ProLeuHisGlnA 45
41 ..... 45
276 CAGAGTTGGATGCCGGAGAGTGATCCCATGCGCAGAGTAAGCAAG 325
   ..... 61
45 IametaArgAlaAlaGlyAspGluPheGluThrArgPheAlaGlyThrPhe 61
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326 CGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 375
   ..... 78
62 SerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGlnAr 78
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376 AGTACCCTGACATCCACACTCCATCAATCAACCCAGGAGAGATTCAGAG 425
   ..... 95
78 gPheThrGlnValSerAspGluLeuPheGlnGlyProAsnTrpGly 95
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
426 CTTGAACAGCTAGTAACTCTCCGCGATGCGGTAAACTGGGCTC 475
   ..... 111
95 rGluValAlaAlaPhePheValPheGlyAlaAlaLeuCysAlaGluSerVal 111
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476 GCATTGTGGCTTTTCTCTTCCTCGGCGGAGCATCTGCTGGAAGCCGTA 525
   ..... 128
112 AsnLysGluMetGluProLeuValGlyGlnValGlnGlnTrpMetValAl 128
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526 GACAGAGGAGATGACAGTATGTGTGATGCGATGCGAGCTGTGAGGCCAC 575
   ..... 145
128 aTyrLeuGluThrArgLeuAlaAspTrpLysHisSerSerGlyTyrPhe 145
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576 TTACCTGATGACACCTAGAGCCTTGATCCAGAGAAAGCGGCTGGG 625
   ..... 161
145 IagLupheThrAlaLeuTyrGlyAspGlyAlaLeuGluGlnAlaArgArg 161
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626 ATACTTTTGTGAACTCTATGGAACATGACAGCCGAGAGCGGAAAG 675
   ..... 176
162 LeuArgGlu.....GlyAsnTrpAlaSerValAlaGlnValLeuThrG 176
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676 GGCAGAGAGAGCTCAACCGCTGTCTCTGAGCGAGCATGACTGTGGCGG 725
   ..... 192
176 yAlaValAlaLeuGlyAlaLeuValThrValGlyAlaPhePheAlaSer 192
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726 CGGTGTTCTGCTGCTGCTCTTTCAGTGGGAAAGCTATTCGTGGGCGC 774

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seq\_name: /SIDS1/gcgdata/geneseq - emb1/NA2001A.DAT:AAH43464

seq\_documentation\_block:

ID AAH43464 standard; CDNA: 702 BP.

AAH43464;

04-DEC-2001 (first entry)

CDNA clone HP03564 ORF.

Npw38; NpwBP; protein interaction; reporter function; eukaryotic cell; localization; protein network; intracellular; primer; amplify; PCR;

KW polymerase chain reaction; mitochondria; ss.

XX Homo sapiens.

OS WO200168885-A1.

PN 20-SEP-2001.

XX 13-MAR-2001; 2001WO-JP01973.

XX 15-MAR-2000; 2000JP-0073095.

XX 24-AUG-2000; 2000JP-0254418.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX Kato S, Eguchi C, Nagata N, Otake M;

XX WPI; 2001-590069/66.

XX P-PSDB; AAB47515.

XX Detection of protein-protein interactions for screening compounds

XX capable of modifying the interaction comprises observing intracellular

XX localization of one protein after altering the modification pattern

XX Example 6; Page 27-29; 33pp; Japanese.

XX This sequence represents the open reading frame of the mitochondrial

XX CDNA clone HP03564. The protein encoded by this sequence was used

XX in the method of the invention. The method allows detection of

XX interactions between a protein X and a protein Y which has a reporter

XX function in eukaryotic cells, and comprises modifying the localization

XX patterns of X and/or Y, and the localization of Y in the cell is

XX observed using the reporter function. This method is useful for the

XX elucidation of protein networks within the cell. It is also applicable

XX for the discovery of new proteins and low-molecular drugs, by

XX observing their effect on intracellular protein interactions.

XX Sequence 702 BP; 165 A; 175 C; 224 G; 138 T; 0 other;

XX alignment\_scores: Quality: 428.50 Length: 224

XX Ratio: 3.018 Gaps: 4

XX Percent Similarity: 63.393 Percent Identity: 40.625

XX alignment\_block:

XX US-09-155-327E-7 x AAH43464

XX Align seg 1/1 to: AAH43464 from: 1 to: 702

XX 11 ArgAlaLeuValAlaAspPheValGlyTyrLysLeuArgGlnLysGlyTyr 27

XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

XX 16 CGGAGAGTGTGGTGTGACTTCTCTCTACAAAGCTTTCACGAAAGGATA 65

XX 27 I..... 27

XX 66 CAGCTGAGTCAGTTAGTATGTGAAAGAACAGAGCTGAGGCCCGAC 115

XX 28 .....ValCysGlyAlaGlyPro 33

XX 116 AAGGAGCTGATCGAGATGAGAGCCCGACGTGCATCAATGCAACCCCA 165

XX 34 .....GlyGluGlyProAlaAlaAsp..... 40

XX 166 TCCTGGCAGCTGGCAGACAGCCCGCGGTGATGAGAGCCCTGCGCACAG 215

XX 41 .....ProLeuHisGlnA 45

XX 216 CAGAGTTGGATGCCGGAGAGTGATCCCATGCGCAGAGTAAGCAAG 265

XX 45 IametaArgAlaAlaGlyAspGluPheGluThrArgPheAlaGlyThrPhe 61

XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

XX 266 CGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 315

62 SeraspLeuAlaIaagLnleuHsVaLlThrProGlySerAlaagLnIar 78  
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316 AGTACCTGCACATCCACAGCTCCACATCCACCAGGAGAACGATATTCAG 365  
78 gPheThrGlnValSeraspLeuPheGlnGlyLysProsnTrpGlyA 95  
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366 CTTTGACACAGGATAGTGAATCACTCTTCGGGGATGGGGTAAACTGGGCTC 415  
95 rGLeuValAlaPhePheValPheGlyAlaAlaLeuCysAlaGluSerVal 111  
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416 GCATTTGGGCGCTTTTCTCTCCCTTCGGGGGGCGACTGCTGGTGAACAGCGTA 465  
112 AsnTyrSGLuMetGluProLeuValGlyGlnValGlnGluTrpMetValAl 128  
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466 GACAAGAGATGCAGGATTTGGTGGAGTCCGATTCGACGTTTGATGGGCGAC 515  
128 aTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerGlyLysTrpA 145  
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516 TTACCTCAAAAGCACCTCTAGACCTGTGGTCAGAGAACGGCGGCTGGG 565  
145 LagLupPheThrAlaLeuArgGlyAspGlyAlaLeuGlnGluAlaArgArg 161  
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566 ATACTTTTGGGAGACTCTATGGGAACAATGACGACGCCGAGAGCCGAAG 615  
161 LeuArgGlu.....GlysnTrpAlaSerValArgThrValLeuTrpG 176  
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616 GGGCAGGAGACGGCTTCAACCGCTGGTTCTCAGCGGCGATCACTGGCCG 665  
176 ValAlaAlaLeuGlyAlaLeu 183  
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666 CGTGCTTTCGCTGGGCTCACCT 667

100

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101 GGGGGGGGGCCAGCAGTGCACCCGCTGCACACAGCAGCGGGGACCTGG 150
51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAla1a1 67
151 GATAGTTCGAGACCCGCTTCGCGCCGACCTCTGATCTGCGCGCTCA 200
67 nLeuHISValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
201 GCTTCATGTGACCCGAGCTCAGCCAGCAGACCTTCACCCAGGTCTCCG 250
84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
251 ACAGACTTTTCAAGGGGGCCCACTGGGGCCGCTTACCTCTCTT 300
101 ValPheGlyAlaAlaLeuGlnGlnSerValAsnValGlnMetGluTrp 117
301 GTCTTTGGGGCTGCACCTGTGTGTGTGAGAGTGTCAACAGAGATGAAAC 350
117 oLeuValGlyGlnValGlnGluTrpMetValAlaTrpLeuGlnTrpArgL 134
351 ACTGTGGGAGCAAGTGCAGAGTGTGATGTGGCTACCTGGAGAGCGGCG 400
134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
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151 TTTGGLYAspGlyAlaLeuGlnGlnAlaArgArgLeuArgGlnGlyAsnTr 167
451 TACGGGGGAGGGGGCCCTGGAGAGGCGCGGCTGCGGGAGGGAACCTG 500
167 pAlaSerValArgThrValIleuThrGlyAlaValAlaLeuGlnValLeu 184
501 GGATCAGTGCAGAGACAGTGTGAGCGGGGGCCGCTGGGACCTGGGCGCT 550
184 aAlhValGlyAlaPhePheAlaSerIys 193
551 TAACTGTAGGGGCTTTTGTCTAGCAAG 579

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seq\_name: gb-pr:BC021198

seq\_documentation block:

LOCUS BC021198 1437 bp mRNA linear PRI 22-JAN-2002

DEFINITION Homo sapiens, BC12-like 2, clone MGC:10675 IMAGE:5944307, mRNA,

ACCESSION BC021198 complete cds.

VERSION BC021198.1 GI:18203706

KEYWORDS MGC.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 1437)

Strausberg,R.

Direct Submission

Submitted (14-JAN-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: http://mgc.ncl.nih.gov

Contact: MGC help desk

Email: c9apbs-remail.nih.gov

Tissue Procurement: DCTD/DTF

CDNA Library Preparation: Rubin Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)

Sequencing Center (NISC),

Gaithersburg, Maryland.

Web site: http://www.nisc.nih.gov/

Contact: nisc\_mgc@nsl.nih.gov

Shevchenko, Y., Wetherby, R.D., Beckstrom-Sternberg, S.M.,

Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,

Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,

REMARK

COMMENT

Lim, M., Maduro, O. L., Masello, C., Mastrian, S. D., McCloskey, J. C., McDowell, J., Pearson, R., Snyder, B., Stantlepp, S., Thomas, P. J., Thongson, E. E., Touchman, J. W., Tsurgeon, C., Vogt, J. L., Walker, M. A., Zhang, L., H. and Green, E. D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov> Series: RAW, Plate: 15 Row: k Column: 19 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14574571.

## FEATURES

source

Location/Qualifiers

1..1437

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/db\_xref="taxon:9606"

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/clone\_id="NIH-MGC-7"

/lab\_host="DH10B-R"

/note="Vector: pOTB7"

176..757

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BASE COUNT 303 a 343 c 509 g 282 t

ORIGIN

alignment\_scores:

Quality: 1007.00

Ratio: 5.218

Percent Similarity: 100.000

Percent Identity: 100.000

alignment\_block:

US-09-155-327e-7 x BC021198 ..

Align seg 1/1 to: BC021198 from: 1 to: 1437

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17 eValGlyTrpLysLeuArgGlnLysGlyTrpValCysGlyAlaGlyProG 34
226 TGTAGGTTATTAAGCTGAGGAGAGGTTATGTCGTGGAGCTGGCCCCG 275
34 LysGlyGlyProAlaAlaAspProLeuGlnGlnAlaMetArgAlaGly 50
276 GGGAGGGCCAGCAGCTGACCCAGCTGACCAAGCAAGTGGGGCAGCTGA 325
51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAla1a1 67
326 GATGAGTTGAGACCCGCTTCGCGCGCACCTTCTGTGATCTGCGCGCTCA 375
67 nLeuHISValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
376 GCTGCTGTGACCCAGGCTCAGCCAGCAGACCTTCACCCAGGCTCCG 425
84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
426 ATGAACCTTTTCAAGGGGGCCCACTGGGGCCGCTTGTGACCTCTTT 475
101 ValPheGlyAlaAlaLeuGlnGlnSerValAsnValGlnMetGluTrp 117
476 GTCTTTGGGGCTGCACCTGTGTGTGTGAGAGTGTCAACAGAGATGAAAC 525
117 oLeuValGlyGlnValGlnGluTrpMetValAlaTrpLeuGlnTrpArgL 134

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526 ACTGTGGGCAAGTCAGAGTGTGCTACTGAGACCGGC 575  
 134 euAlaasprtrpIleHisSerSerGlyTTPAlaGluPheThrAlaLeu 150  
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 151 TyrGlyAspGlyAlaLeuGluGluAlaArgAlaArgGluGlyAsnTr 167  
 626 TACGGGACGGGGCCCTGGAGGAGCGCGCTGCGGAGGAGACTG 675  
 167 palAservalArgThrValIleuThrGlyAlaValAlaLeuGlyAlaLeu 184  
 676 GGCATCAGTCAGAGCAGTCTGACGGGGCCGCGCAGTGGGCCCTGG 725  
 184 alThrValGlyAlaPhePheAlaSerLys 193  
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seq\_name: gb\_pr.D87461

seq\_documentation\_block:

LOCUS D87461 3542 bp mRNA linear PRI 06-OCT-2001  
 DEFINITION Human mRNA for KIAA0271 gene, complete cds.

ACCESSION D87461  
 VERSION D87461.1 GI:1944417  
 KEYWORDS KIAA0271.  
 SOURCE Homo sapiens male brain myoblast cell\_line:KG-1 cDNA to mRNA,  
 clone.lib:PSPORT 1 clone:HA6752.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

Nagase,T., Seki,N., Ishikawa,K., Ohira,M., Kawarabayashi,Y.,  
 Ohara,O., Tanaka,A., Kotani,H., Miyajima,N. and Nomura,N.  
 Prediction of the coding sequences of unidentified human genes. VI.  
 The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by  
 analysis of cDNA clones from cell line KG-1 and brain

TITLE

JOURNAL DNA Res. 3 (5), 321-329 (1996)

MEDLINE 97191544

2 (bases 1 to 3542)

REFERENCE Ohara,O., Nagase,T., Kikuno,R. and Nomura,N.

AUTHORS

TITLE

Submitted (27-AUG-1996) Osamu Ohara, Kazusa DNA Research Institute;  
 1532-3, Yata, Kisarazu, Chiba 292-0812, Japan  
 (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)

JOURNAL

FEATURES

source

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Quality: 1007.00 Length: 193  
 Ratio: 5.218 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-327e-7 x D87461 ..

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 34 LysGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaIaGly 50  
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seq\_name: gb\_pat.AR020780

seq\_documentation\_block:

LOCUS AR020780 579 bp DNA linear PAT 05-DEC-1998  
 DEFINITION Sequence 2 from patent US 5789201.

ACCESSION AR020780

VERSION AR020780.1 GI:3975395

KEYWORDS

SOURCE

ORGANISM

AUTHORS

TITLE

JOURNAL

FEATURES

1 (bases 1 to 579)

Genes coding for bcl-2 and bcl-2 homologue  
 Patent: US 5789201-A 2 04-AUG-1998;  
 Location/Qualifiers

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  Ratio: 5.219          Gaps: 0
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alignment_block:
  US-09-155-327e-7 x AR020780
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51 TGTAGCTTATAGCTGACGACAGAGGCTTATGCTGTGGAGCTGGCCCG 100
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184 AlThrValGlyAlaPhePheAlaSerLys 193
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551 TAACTGATAGGGGCGCTTTTGTGACGACAG 579
seq_name: gb_ro:MM059746
seq_documentation_block:
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DEFINITION     Mus musculus Bcl-w (bcl-w) mRNA, complete cds.
ACCESSION      U59746
VERSION        059746.1  GI:1572494
KEYWORDS
SOURCE          house mouse.

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ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 582)
AUTHORS
Gibson, L., Holmgren, S. P., Huang, D. C., Bernard, O., Copeland, N. G.,
Jenkins, N. A., Sutherland, G. R., Baker, E., Adams, J. M. and Cory, S.
JOURNAL
Oncogene 13 (4), 665-675 (1996)
MEDLINE
96358615
REFERENCE
2 (bases 1 to 582)
AUTHORS
Gibson, L., Holmgren, S. P., Huang, D. C., Bernard, O., Adams, J. M. and
Cory, S.
TITLE
Direct Submission
JOURNAL
Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and
Eliza Hall Institute of Medical Research, PO Royal Melbourne
Hospital, Parkville, Victoria 3050, Australia
FEATURES
source
1..582
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="14"
/cell_line="BaF3"
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/gene="bcl-w"
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RLREGMNASRYTLGAVVALVGVAFPFASK"
BASE COUNT      107 a 158 c 200 g 117 t
ORIGIN
alignment_scores:
  Quality: 1000.00      Length: 193
  Ratio: 5.181          Gaps: 0
  Percent Similarity: 100.00  Percent Identity: 98.964
alignment_block:
  US-09-155-327e-7 x MM059746
Align seg 1/1 to: MM059746 from: 1 to: 582

1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
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1 ATGGCGACCCCGACGCTCAACCCGACAGCGGGGCTGTGTGCTGACTT 50
17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProg 34
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51 TGTAGCTTATAGCTGACGACAGAGGCTTATGCTGTGAGCTGGCCCTG 100
34 lYgLuGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
|||||
101 GGGAGGGCCCGACGCGCGACCCGCTGACCAACCCATGGGGGCTGCTGGA 150
51 AspGluPheGluThrArgPheArgThrPheSerAspLeuAlaAlaGly 67
|||||
151 GACGAGTTGAGACCCGCTTCCGCCGACCTTCTGTGACTTGGCCGCTCA 200
67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSera 84
|||||
201 GCTACACAGTACCCCGACGCTGACCCAGCAGCTTCAACCCAGGTTTCG 250
84 sPGLuLeuPheGlnGlnGlyLysProAsnTrpGlyArgLeuValAlaPhePhe 100
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251 ACGAACTTTTCCAAAGGGGCGCTTAACCTGGGGGCGCTTGTGCAATCTTT 300

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seq\_name: gb\_pat:AX022529

seq\_documentation\_block:

LOCUS AX022529 583 bp DNA linear PAT 07-SEP-2000

DEFINITION Sequence 6 from Patent EP0932674.

ACCESSION AX022529

VERSION AX022529.1 GI:10046125

KEYWORDS

SOURCE unidentified.

ORGANISM unidentified.

REFERENCE 1 (bases 1 to 583)

AUTHORS Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.

TITLE A novel mammalian gene, bcl-w, belongs to the bcl-2 family of

JOURNAL apoptosis-controlling genes

AMRAD OPERATIONS PTY LTD (AU)

FEATURES

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/note="unnamed protein product"

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GAALCAESVKNKEPPLVGYOEMWVAYLETRLVDMIHSSGMAEFTALYGDGALEEAR

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BASE COUNT 105 a 157 c 210 g 111 t

ORIGIN

alignment\_scores:

Quality: 1000.00 Length: 193

Ratio: 5.181 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 98.964

alignment\_block:

US-09-155-327E-7 x AX022529 ..

Align seg 1/1 to: AX022529 from: 1 to: 583

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1 ATGGGACCCCAAGCTCGGCCACAGACAGCGGCTGTGGGCAAGACTT 50

17 eValGlyTyrLysLeuArgInLysGlyTyrValCysGlyAlaGlyProG 34

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51 TGTAGCTTATAAGCTGAGCAGGAGGCTTATCTGTGGAGCTGGCCCCG 100

34 TGTAGCTTATAAGCTGAGCAGGAGGCTTATCTGTGGAGCTGGCCCCG 150

101 GGGAGGCCCCAGCAGCTGACCCGCTGACCAAGCCATGCGGGAGCTGGA 150

51 AspGluPheGluThrArgPheArgThrPheSerAspLeuAlaGlu 67

151 GATGAGTTTCAGACCCGCTTCCGGGCACTTCTGTATCTGGCGGCTCA 200

67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSer 84

201 GCTGCATGAGCCCAAGCTCAGCCACCAAGCCATGACCCAGGCTTCG 250

84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100

251 ACGAACCTTTTCAAGGGAGGCCCAACTGGGGCCGCTGTAGCTTCTTT 300

101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluP 117

301 CTCTTTGGGGCTGCACTGTGCTGAGAGTCAACAAGAGAGATGGAAC 350

117 OleuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArg 134

351 ACTGTGGGACAAAGTGCAGAGTGTGATGCTTACCTGAGACGCGCG 400

134 eulAlaSprPrlIleHisSerSerGlyTyrPAlaGluPheThrAlaLeu 150

401 TGGTCAGCTGATCCACAGCAGTGGGGCTGGCGGAGTTCACAGCTCTA 450

151 TyrGlyAspGlyAlaLeuGluGlnAlaArgArgLeuArgGluGlyAsnTr 167

451 TACGGGAGCGGGCCCTCGAGAGCGCGCGCTCGCGGAGGGAACG 500

167 PalAserValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeu 184

501 GGCATCAGTAGAGACAGTCTGACGCGGGCCGTGGCAGCTGGGGGCTTG 550

184 alThrValGlyAlaPhePheAlaSerLys 193

551 TAACTGTAGGGGCTTTTGTGTAACAAG 579

seq\_name: gb\_pat:AX030817

seq\_documentation\_block:

LOCUS AX030817 583 bp DNA linear PAT 20-SEP-2000

DEFINITION Sequence 6 from Patent WO9735971.

ACCESSION AX030817

VERSION AX030817.1 GI:10278311

KEYWORDS

SOURCE unidentified.

ORGANISM unidentified.

REFERENCE 1 (bases 1 to 583)

AUTHORS Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.

TITLE A novel mammalian gene, bcl-w, belongs to the bcl-2 family of

JOURNAL apoptosis-controlling genes

PATENT: WO 9735971-A 6 02-OCT-1997;

ADAMS JERRY MCKEE (AU); HOLMGREEN SHARON P (AU); CORY SUZANNE (AU)

GIBSON LEONIE M (AU); AMRAD OPERATIONS PTY LTD (AU)

FEATURES

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BASE COUNT 105 a 157 c 210 g 111 t  
 ORIGIN

## alignment\_scores:

Quality: 1000.00 Length: 193  
 Ratio: 5.181 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 98.964

## alignment\_block:

US-09-155-327e-7 x AX030817 ..

Align seg 1/1 to: AX030817 from: 1 to: 583

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1 ATGGGACCCAGCCAGCTCGGCCCCAGACACAGCGGCTCGTGGCGAGACTT 50
17 eValGlyTyrLysLeuArgGlnLysGlyTyrValAlcysGlyAlaGlyProG 34
1 TTAGGCTATTAAGCTGAGCAGAGAGGTTATGTCTGTGAGACTGGCCCCG 100
34 LysGlnGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
101 GGGAGGGCCAGCAGCTGACCCGCTGCACCAAGCCATCGGGCGAGCTGGA 150
51 AspGluPheGluThrArgPheArgThrPheSerAspLeuAlaAlaGly 67
151 GATGAGTTGAGACACCGGCTCGGCGCACCTTCTGTGATGCTGGCGCTCA 200
67 nLeuHisValThrProGlySerAlaGlnAlaArgPheThrGlnValSerA 84
201 GGTGATGTGACCCAGCTCAGCCAGCAAGCGCTCACCGAGGTCTCGG 250
84 spGluLeuPheGlnGlyLysProAsnTrpGlyArgLeuValAlaPhePhe 100
251 ACGAACTTTTCAAGGGGGCCCAACTGGGCCCTTGTAGCTTCTTT 300
101 ValPheGlyAlaAlaLeuCysAlaGlnSerValAsnLysGlnMetGluPr 117
301 CTTCTTGGGGCTGCACCTGTGTGCTGAGAGTGTCAACAAGAGATGAGAAC 350
117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
351 ACTGCTGGGACAGAGTGAGAGTGATGTGCTTACTTGAAGACGGCGC 400
134 euAlaAspTrpIleHisSerSerGlyLysTyrPalaGluPheThrAlaLeu 150
401 TGTCGACTGATCCACAGCAGTGGGGCTGGCGGAGTTCCACAGCTCTA 450
151 TyrGlyAspGlyAlaLeuGlnGluAlaArgArgLeuArgGlnLysAsnTr 167
451 TACGGGGACGGGGCCCTGGAGAGAGCGCGCTCGGGAGGGAACCTG 500
167 palSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
501 GGCATCAGTGAAGAGTCTGACGGGGCGCGTGGGACACTGGGGCCCTTG 550
184 alThrValGlyAlaPhePheAlaSerLys 193
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seq\_name: gb\_ro:AF030769

seq\_documentation\_block:

LOCUS AF030769 3476 bp mRNA linear ROD 16-NOV-1997  
 DEFINITION Mus musculus BCL-W (Bcl-w) mRNA, complete cds.  
 ACCESSION AF030769  
 VERSION AF030769.1 GI:2623249

KEYWORDS  
 SOURCE house mouse.  
 ORGANISM Mus musculus

## REFERENCE

1 (bases 1 to 3476)  
 Ross, A.J., Waymire, K.G., Moss, J.E., Palow, A.F., Russell, L.D. and Macgregor, G.R.  
 Bcl-w is required for testis homeostasis

2 (bases 1 to 3476)  
 Ross, A.J. and Macgregor, G.R.  
 Direct Submission

## JOURNAL

Submitted (21-OCT-1997) Center for Molecular Medicine, Emory University, 1462 Clifton Road, Atlanta, GA 30322, USA

## FEATURES

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 /strain="C57BL/10J"  
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## exon

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Quality: 1000.00 Length: 193  
 Ratio: 5.181 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 98.964

## alignment\_block:

US-09-155-327e-7 x AF030769 ..

Align seg 1/1 to: AF030769 from: 1 to: 3476

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1 TTAGGCTATTAAGCTGAGCAGAGAGGTTATGTCTGTGAGACTGGCCCCG 278
229 TGTAGGCTATTAAGCTGAGCAGAGAGGTTATGTCTGTGAGACTGGCCCCG 278
34 LysGlnGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
101 GGGAGGGCCAGCAGCTGACCCGCTGCACCAAGCCATCGGGCGAGCTGGA 328

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TITLE  
 DIRECT JOURNAL  
 Submitted (01-OCT-1998). Developmental Neuroscience, Uppsala  
 University, Box 587, BMC, Uppsala 751 23, Sweden  
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 Location/Qualifiers  
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GAALCAESVKNEMEPVGVQVDMVIVLETRLADWTHSSGMAEFALYGDALAEAR  
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BASE COUNT 111 a 157 c 200 g 114 t  
ORIGIN

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quality: 996.00 Length: 193  
Ratio: 5.161 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 98.446

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US-09-155-327E-7 x AF096291 ..

Align seg 1/1 to: AF096291 from: 1 to: 582

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1 ATGGGGACCCCGAGCTCAACCCGACACACGCGCTCTAGTGGCTGACTT 50
17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyPro 34
51 TGTAGGCTATAGCTGAGGAGCAAGGGTTATGCTGTGAGAGCTGGCCCTG 100
34 LysGlyGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
101 GGGAAAGGCCCGACAGCCGAGCCGCTGACCAAGCCATGCGGAGCGTGA 150
51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaGly 67
151 GACGAGTTTGAGACCCGCTTCCGGGCACTTCTCTACCTGGCCGCTCA 200
67 nLeuHisValThrProGlySerAlaGlnAlaArgPheThrGlnValSer 84
201 GCTACAGCTGACCCAGGCTCAGCCGCAACGCTTCACCCAGGTTTCCG 250
84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
251 ACGAACTTTTCCAAAGGGGGCCCCAACAGTGGGGCGCTGTGGCATTCCTT 300
101 ValPheGlyAlaAlaLeuGlyAlaGluSerValAsnLysGluMetGluP 117
301 GTCTTTGGGGCTGCGCTGTGCTGAGAGTGTCAACAAGAATATGAGCC 350
117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArg 134
351 ATTGGTGGGACAAAGTGCAGGATTGATGTGACCTCCTGAGACACGCT 400
134 euAlaAspTrpLeuHisSerSerGlyTyrTrpAlaGluPheThrAlaLeu 150
401 TGGCTGACGATCCACAGCAGTGGGGCTGGGGGAGATTCACAGCTCTA 450
151 TyrGlyAspGlyAlaLeuGluGlnAlaArgArgLeuArgGluGlyAsnTr 167
451 TACGGGACCGGGGCGCTGAGAGGACGCGCTTGGGAGGAGGACG 500
167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeu 184
501 GGCATGAGTGAAGACAGTGTCTAGCGGGGCTGTGGCACTGGGGCCCTCG 550

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184 aThrValGlyAlaPhePheAlaSerLys 193  
551 TAACTGTAGGGCGCTTTTGTGTAGCAAG 579

seg\_name: gb\_pat:AX022531

seg\_documentation\_block:

LOCUS AX022531 581 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 8 from Patent EP0932674.  
ACCESSION AX022531  
VERSION AX022531.1 GI:10046127  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

unidentified.  
unclassified.  
1 (bases 1 to 581)  
Adams,J.M., Holmgren,S.P., Cory,S. and Gibson,L.M.  
A novel mammalian gene, bcl-w, belongs to the bcl-2 family of  
apoptosis-controlling genes  
Patent: EP 0932674-A 8 04-AUG-1999;  
AMRAD OPERATIONS PTY LTD (AU)  
location/Qualifiers  
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CDS

BASE COUNT 105 a 164 c 195 g 117 t  
ORIGIN

## alignment\_scores:

Quality: 965.00 Length: 193  
Ratio: 5.079 Gaps: 0  
Percent Similarity: 98.446 Percent Identity: 94.819

## alignment\_block:

US-09-155-327E-7 x AX022531 ..

Align seg 1/1 to: AX022531 from: 1 to: 581

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67 nLeuHisValThrProGlySerAlaGlnAlaArgPheThrGlnValSer 84
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84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
251 ACGAACTTTTCCAAAGGGGGCCCCAACAGTGGGGCGCTGTGGCACTGG 300

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Center code: GS  
Web site: <http://www.genoscope.cns.fr/>  
Contact: [Sequref@genoscope.cns.fr](mailto:Sequref@genoscope.cns.fr)

The following BAC sequence is oriented from the T7 to the SP6 end.  
Upstream BAC (overlapping the T7 end) : R-244E17  
Downstream BAC (overlapping the SP6 end) : C-2201G16 (AC=AL132855)

Summary Statistics  
Assembly program: Phrap; version 2.0  
Quality coverage: 7.94x in Q20 bases; sum-of-contigs

# Overall quality chart :

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Range : bases
0
1 - 9
10 - 19
20 - 29
30 - 39
40 - 49
50 - 59
60 - 69
70 - 79
80 - 89
90 - 99
111256

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Percentage of bases with a quality value >= 40 : 99 %.

## Location/Qualifiers

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dbSTS:STS69699
Identified using the e-PCR software (G. Schuler)"
80433. 80566
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82164. 82299
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Identified using the e-PCR software (G. Schuler)"

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Rdb:RH9543

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Rdb:RH28416

dbSTS:STS20162

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Identified using the e-PCR software (G. Schuler)"

194804. 194903

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Rdb:RH76320

dbSTS:STS53407

Identified using the e-PCR software (G. Schuler)"

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BASE COUNT

ORIGIN

alignment\_scores:

Quality: 873.50

Ratio: 4.526

Percent Similarity: 48.371

Percent Identity: 47.870

alignment\_block:

US-09-155-327e-7 x CNS0000B

Align seg 1/1 to: CNS0000B from: 1 to: 196292

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34 TGTGCTTATAAGCTGAGCAGAGGGTTATGCTGTGGAGCTGGCCCC 89975

89926 GGGAGGGCCAGCAGCTGACCCGACACAGCCATCGGGCAGCTGCA 89975

51 AspGluPheGluThrArgPheArgThrPheSerAspLeuAlaAlaG 67

89976 GATGAGTTTGAGACCCGCTTCGGCGCACCTTCTGTGATGGCGCTCA 90025

67 nLeuHisValThrProGlySerAlaGlnAlaArgPheThrGlnValSer 84

90026 GCTGATGTGACCCAGGCTGACCCACAGCGCTTACCCAGGCTCTCG 90075

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  Rattus norvegicus chromosome 4 clone Rp1-246H18 strain Brown
  DEFINITION
  Norway, WORKING DRAFT SEQUENCE, 5 unordered pieces.
ACCESSION
AC079885
VERSION
AC079885.2 GI:11120768
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Norway rat.
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 151212)
Beckstrom-Stenberg,S.M., Benjamin,B., Blakesley,R.W.,
Bouffard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Gupta,J.,
Ho,S.-L., Idol,J., Karlins,E., Lee-Edn,S.-O., Legaspi,R., Lim,M.,
Maduro,O.L., Maduro,V.B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Prasad,A., Snyder,B., Stantiripop,S.,
Thomas,J.W., Thomas,P.J., Tjongson,E.E., Touchman,J.W.,
Tsurgoun,C., Vogt,J.L., Walker,M.A., Wetherby,K.D. and Green,E.D.
NISC Mouse Sequencing Initiative
Unpublished
2 (bases 1 to 151212)
Green,E.D.
Direct Submission
Submitted (16-SEP-2000) NIH Intramural Sequencing Center, 8717
Groversom Circle, Galthersburg, MD 20877, USA
On Nov 8, 2000 this sequence version replaced gi:10179358.
----- Genome Center

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## Source

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/strain="Brown Norway"
/db_xref="taxon:10116"

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Submitted (16-SEP-2000) NIH Intramural Sequencing Center, 8717  
 Rockledge Drive, Bethesda, MD 20877, USA gi:10179358.  
 v. 8, 2000 this sequence version replaced  
 Genome Center  
 Center: NIH Intramural Sequencing Center  
 Center code: NISC  
 Web site: <http://www.nisc.nih.gov>  
 Contact: [nisc.mouse@nihgri.nih.gov](mailto:nisc.mouse@nihgri.nih.gov)  
 Project Information  
 Center project name: rx  
 Center clone name: 246H18  
 Summary Statistics  
 Sequencing vector: plasmid; n/a; 100% of reads  
 Chemistry: dye-terminator; Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 147800 bases at least Q40  
 Consensus quality: 148726 bases at least Q30  
 Consensus quality: 149333 bases at least Q20  
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 Insert size: 150812; sum-of-conflicts  
 Insert coverage: 11.76x in Q20 bases; agarose-*fp*  
 Quality coverage: 11.30x in Q20 bases; sum-of-conflicts



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                 clone_end:T7
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ORIGIN
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    Percent Similarity: 86.528    Percent Identity: 69.430
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49829 .....GCTGGCCCCG 49838
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RESULT 2  
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 : Sequence 1, Application US/08978523  
 : Patent No. 5883229  
 :  
 : GENERAL INFORMATION:  
 : APPLICANT: Gusestella, John  
 : TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
 : TITLE OF INVENTION: Homologue  
 : NUMBER OF SEQUENCES: 53  
 :  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 : STREET: 1100 New York Avenue, N.W., Suite 600  
 : CITY: Washington  
 : STATE: DC  
 : COUNTRY: USA  
 : ZIP: 20005  
 :  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.30  
 :  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/978,523  
 : FILING DATE: herewith  
 : CLASSIFICATION:  
 :  
 : PRIORITY APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/798,897  
 : FILING DATE: February 11, 1997  
 : CLASSIFICATION: 424  
 :  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Esmond, Robert W.  
 : REGISTRATION NUMBER: 32,893  
 : REFERENCE/DOCKET NUMBER: 1483.0140002  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 202-371-2500  
 : TELEFAX: 202-371-2540

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? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 579 base pairs
? type: nucleic acid
? STRANDEDNESS: both
? TOPOLOGY: both
? MOLECULE TYPE: cdna
? US-08-978-523-1

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Matches 566; Conservative	0;	Mismatches 13;	Indels 0;	Gaps 0;

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RESULT 3  
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 : Sequence 2, Application US/08798897  
 : Patent No. 5789201  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: Guastella, John  
 :  
 : TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2  
 : TITLE OF INVENTION: Homologue  
 :  
 : NUMBER OF SEQUENCES: 53  
 :  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESS: STERNER, KESSLER, GOLDSTEIN & FOX P. L.L.C  
 : STREET: 1100 New York Avenue, N.W., Suite 600  
 : CITY: Washington  
 : STATE: DC  
 :  
 : COUNTRY: USA  
 :  
 : ZIP: 20005  
 :  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/798,897  
 FILING DATE: February 11, 1997  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Esmond, Robert W.  
 REGISTRATION NUMBER: 32,893  
 REFERENCE/DOCKET NUMBER: 1483.0140001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-2600  
 TELEFAX: 202-371-2540  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 579 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: both  
 MOLECULE TYPE: cDNA  
 US-08-798-897-2

Query Match 88.5%; Score 515; DB 1; Length 579;  
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RESULT 4  
 US-08-978-523-2  
 Sequence 2, Application US/08978523  
 Patent No. 5883229

GENERAL INFORMATION:  
 APPLICANT: Guastella, John  
 TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2  
 TITLE OF INVENTION: Homologue  
 NUMBER OF SEQUENCES: 53  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 STREET: 1100 New York Avenue, N.W., Suite 600  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/978,523  
 FILING DATE: herewith  
 CLASSIFICATION: 424  
 PRIOR APPLICATION NUMBER: US 08/798,897  
 APPLICATION NUMBER: 1483.0140002  
 FILING DATE: February 11, 1997  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Esmond, Robert W.  
 REGISTRATION NUMBER: 32,893  
 REFERENCE/DOCKET NUMBER: 1483.0140002  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-2600  
 TELEFAX: 202-371-2540  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 579 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: both  
 MOLECULE TYPE: cDNA  
 US-08-978-523-2

Query Match 88.5%; Score 515; DB 2; Length 579;  
 Best Local Similarity 93.1%; Pred. No. 1.4e-131;  
 Matches 539; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

OY 1 atggcgaccccaagcctcaaccccaagacacacagcgtctagctgactgtagctat 60  
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 Db 1 ATGGCGACCCCAAGCCTCAACCCCAAGACACACAGCGTCTAGCTGACTGTTAGCTTAT 60  
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Best Local Similarity	58.3%	Pred

Query Match	23.1%;	Score 134.6;	DB 2;	Length 926;
Best Local Similarity	58.3%;	Pred. NO. 8.7e-28;		
Matches 236; Conservative	0;	Mismatches 169;	Indels 0;	Gaps 0;

LOCATION: 135..836

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DB 514 tgaatgaactctccgggagtggttaactgggtgcgacttggcttcttctctctg 573  
QY 308 gggctgcccctgtgtctgagagtgtaacaaagaaagggcccttggggagagagtc 367  
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QY 368 aggatgtgagtggtgctaccctggagacacgtctgtgctgactgtatccacagatgagc 427  
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RESULT 9  
US-09-277-020-39  
Sequence 39, Application US/09277020  
Patent No. 6210892  
GENERAL INFORMATION:  
APPLICANT: Bennett, C. Frank  
TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation  
FILE REFERENCE: ISPH-0339  
CURRENT APPLICATION NUMBER: US/09/277.020  
CURRENT FILING DATE: 1999-03-26  
EARLIER APPLICATION NUMBER: 09/167.921  
EARLIER FILING DATE: 1998-10-07  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 39  
LENGTH: 926  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-277-020-39

Query Match 23.1%, Score 134.6, DB 4, Length 926;  
Best Local Similarity 58.3%, Pred. No. 8,7e-28;  
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;  
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DB 394 agcaagcgctgagggagcgacgaggttggacgtggtacgcggcggtcattcagt 453  
QY 188 acctggccgtcagctacacgttgaccacaggtcagccacagccttaccaggttt 247  
DB 454 acctgacatccacgtccacatcaaccacagggagacagatagaggttggacaggtag 513  
QY 248 ccagcagcttcccaagggggccctaccctggggccgtcttggggacacttcttcttg 307  
DB 514 tgaatgaactctccgggagtggttaactgggtgcgacttggcttcttctctctg 573  
QY 308 gggctgcccctgtgtctgagagtgtaacaaagaaagggcccttggggagagagtc 367  
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RESULT 10  
US-09-323-743-1  
Sequence 1, Application US/09323743  
Patent No. 6214986  
GENERAL INFORMATION:  
APPLICANT: Bennett, C. Frank  
APPLICANT: Dean, Nicholas M.  
APPLICANT: Monia, Brett P.  
APPLICANT: Nickoloff, Brian J.  
APPLICANT: Zhang, Qiongling  
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression  
FILE REFERENCE: ISPH-0368  
CURRENT APPLICATION NUMBER: US/09/323.743  
CURRENT FILING DATE: 1999-06-01  
EARLIER APPLICATION NUMBER: 09/277.020  
EARLIER FILING DATE: 1998-03-26  
EARLIER APPLICATION NUMBER: 09/167.921  
EARLIER FILING DATE: 1998-10-07  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 1  
LENGTH: 926  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (135)..(836)  
PUBLICATION INFORMATION:  
DATABASE ACCESSION NUMBER: L20121 Genbank  
DATABASE ENTRY DATE: 1994-07-26  
US-09-323-743-1

Query Match 23.1%, Score 134.6, DB 4, Length 926;  
Best Local Similarity 58.3%, Pred. No. 8,7e-28;  
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QY 188 acctggccgtcagctacacgttgaccacaggtcagccacagccttaccaggttt 247  
DB 454 acctgacatccacgtccacatcaaccacagggagacagatagaggttggacaggtag 513  
QY 248 ccagcagcttcccaagggggccctaccctggggccgtcttggggacacttcttcttg 307  
DB 514 tgaatgaactctccgggagtggttaactgggtgcgacttggcttcttctctctg 573  
QY 308 gggctgcccctgtgtctgagagtgtaacaaagaaatgagccttggggagagagtc 367  
DB 574 gcggggacactgtgtgtgaaagcgtaacaaagagatgcgggattgtgtgagtcgac 633  
QY 368 aggatgtgagtggtgctaccctggagacacgtctgtgctgactgtatccacagatgagc 427  
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QY 428 gctggggagagttacagccttaccggggagcgcccttgagagggagcgagtcgtgc 487  
DB 694 gctgggatacttctgtggaactctatggaacaaatgacacagccggagagccgaaggcc 753  
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Db 754 AGGAACGCTTCAACCGCTGTGCTGACGCGCATGACTGTGCGCG 798

## RESULT 13

US-08-465-485A-20

Sequence 20, Application US/08465485A  
Patent No. 5831066  
GENERAL INFORMATION:  
APPLICANT: Reed, John  
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
ADDRESS: P.C.  
STREET: 1755 S. Jefferson Davis Hwy., Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,485A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/124,256  
FILING DATE: 20-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/840,716  
FILING DATE: 21-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/288,692  
FILING DATE: 22-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Fortney, Andrew D.  
REGISTRATION NUMBER: 34,600  
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (408) 436-2070  
TELEFAX: (408) 436-2075  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 717 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..717  
US-08-465-485A-20

Query Match 20.9%; Score 121.8; DB 2; Length 717;  
Best Local Similarity 58.4%; Pred. No. 2.5e-24;

Matches 213; Conservative 0; Mismatches 152; Indels 0; Gaps 0;  
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QY 151 gacgagtttgagaccggttccgcgcaccttctctgaccttgcgcgctcaagctacagtg 210  
Db 304 GACGACTTCTCCCGCCGCTACCGGCGGACTTGCAGATGTCAGACGAGCTGACACTG 363  
QY 211 acccagagctcagccagcagcagcttccacaggttccgagcaacttctcaaggggagc 270  
Db 364 AGCCCTTCAACCGCGCGGCGGAGCGCTTTGCCACGCTGTGAGAGAGCTTTCAGGAGCGG 423  
QY 271 cctactggggcgctctgtgtgcatcttctcttggggctgacctgtgtgtgagatc 330  
Db 424 GTGACTGGGGAGAGATGTGGCTTCTTGAAGTGTGGGTCATGTTGTGAGAGC 483  
QY 331 gtacacaaagaatgagacgttctgtgtggacaagtgacagatltgatgtgacctactg 390  
Db 484 GTCAACCGGAGAGATGTGGCTTCTTGAAGTGTGGGTCATGTTGTGAGAGC 543  
QY 391 gagacagctgtgtgtgtgatccacagcagtgcgctggcgagtgacagctcta 450  
Db 544 AACCGGACCTGACACACTGATCCAGATTAACGAGGCTGGGATGCTTGTGGAAGT 603  
QY 451 tacgg 455  
Db 604 TACGG 608

## RESULT 14

US-09-080-285-20

Sequence 20, Application US/09080285  
Patent No. 6040181  
GENERAL INFORMATION:  
APPLICANT: Reed, John  
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
ADDRESS: P.C.  
STREET: 1755 S. Jefferson Davis Hwy., Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/080,285  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/465,485  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/124,256  
FILING DATE: 20-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/840,716  
FILING DATE: 21-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/288,692  
FILING DATE: 22-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Fortney, Andrew D.  
REGISTRATION NUMBER: 34,600  
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (408) 436-2070  
TELEFAX: (408) 436-2075  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 717 base pairs





Thu Jun 6 16:39:25 2002

us-09-155-327e-8.rni

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Page 10

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OW nucleic - nucleic search, using sw model

Run on: June 6, 2002, 11:24:29 ; Search time 2348.74 Seconds  
(without alignments)  
3344.443 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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1: em\_estbta:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estlmu:\*  
5: em\_estcov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_estl:\*  
10: gb\_estl2:\*  
11: gb\_hlc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vtl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	495.6	85.2	1030	10 BE793530	BE793530 601590016
5	445	76.5	815	10 BF785386	BF785386 602111728
6	430.6	74.0	697	10 BF770566	BF770566 603060362
7	429.6	73.8	854	11 AK013244	AK013244 Mus muscu
8	417	71.6	792	10 BG298789	BG298789 602396527
9	411.6	70.7	540	9 AM258810	AM258810 um74402.Y
10	366.8	63.0	643	10 BI910270	BI910270 603069493
11	325.4	55.9	362	9 AA596919	AA596919 v021f08.T
12	286.8	49.3	758	10 BI764428	BI764428 603050701
13	277.4	47.7	457	9 BB856021	BB856021 BB856021
14	254.2	42.4	749	10 BG677345	BG677345 602624059
15	246.8	42.4	601	10 BF204905	BF204905 601866718
16	233.6	40.1	433	9 AM326901	AM326901 20104 MAR
17	214.6	36.9	473	10 BE647090	BE647090 UT-M-BH1-

18	204.6	35.2	601	10 BM191403	BM191403 da186a10.
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25	138.2	23.7	624	9 BE188975	BE188975 db62a05.x
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30	132.2	22.7	699	10 BE870269	BE870269 601447403
31	131.2	22.5	697	10 BI457116	BI457116 601185360
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## ALIGNMENTS

RESULT 1	AK015644	1949 bp	mRNA	linear	HTC 19-JAN-2002
LOCUS	AK015644				
DEFINITION	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930488D08:Bcl2-like 2, full insert sequence.				
ACCESSION	AK015644				
VERSION	AK015644.1	GI:12854052			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (strain: C57BL/6J) adult male testis cDNA to mRNA, clone:4930488D08.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
AUTHORS	Carninci, P., and Hayashizaki, Y.				
TITLE	1 (sites)				
JOURNAL	High-efficiency full-length cDNA cloning				
MEDLINE	Meth. Enzymol. 303, 19-44 (1999)				
PUBMED	99279253				
REFERENCE	103499636				
AUTHORS	2 (sites)				
TITLE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.				
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
MEDLINE	Genome Res. 10 (10), 1617-1630 (2000)				
PUBMED	20499374				
REFERENCE	11042159				
AUTHORS	3 (sites)				
TITLE	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasliwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.				
JOURNAL	RIKEN integrated sequence analysis (RISA) system--384-format				
MEDLINE	Genome Res. 10 (11), 1757-1771 (2000)				
PUBMED	20530913				



**MEDLINE** 2049374  
**PUBMED** 11042159  
**REFERENCE** 3 (sites)  
**AUTHORS** Shibata, K., Itoh, M., Mizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komou, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Matsura, S., Saitani, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Ohtsuka, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
**TITLE** RIKEN integrated sequence analysis (RISA) system—384-format sequencing pipeline with 384 multicapillary sequencer  
**JOURNAL** Genome Res. 10 (11), 1757-1771 (2000)  
**MEDLINE** 20530913  
**PUBMED** 11076861  
**REFERENCE** 4 (sites)  
**AUTHORS** The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
**TITLE** Functional annotation of a full-length mouse cDNA collection  
**JOURNAL** Nature 409, 685-690 (2001)  
**REFERENCE** 5 (bases 1 to 3487)  
**AUTHORS** Adachi, T., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Nakagawa, T., Bairdrell, R., Brown, R., Brownstein, M., Bull, C.,

4 (sites)  
THE RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)  
5 (bases 1 to 3487)  
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A.,  
Arakawa, T., Balgarelli, R., Bono, H., Brownstein, M., Bull, C.,  
Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T.,  
Hara, A., Hayasato, N., Hill, D., Hiramoto, K., Hiraoka, T., Horii, F.,  
Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T.,  
Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S.,  
Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K.,  
Nishizaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J.,  
Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,  
Schmidt, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T.,  
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,  
Tanaka, T., Tejima, Y., Toyo, T., Yamamura, T., Yamanaka, I.,  
Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and  
Yasushiro, Y.

**TITLE** Direct Submission  
**JOURNAL** Submitted (10-JUL-2000) yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama 230-0045, Japan (E-mail:genome.res@sc.riken.go.jp, URL:<http://genome.gsc.riken.go.jp/>, Tel:81-45-503-9222, Fax:81-45-503-9216)  
**COMMENT** Please visit our web site (<http://genome.gsc.riken.go.jp/>) for

further details. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGGAGAGAGCGCCGCAACGTCAGATCTTTTCTTTTCTTNN 3'], cDNA was prepared by using reverse transcriptase thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adaptor of sequence [5' GAGGAGAGAGAGATCCCAAGGCTCATTTATTTAAATTAACCCCCCCC 3']. cDNA was cleaved with XhoI and SclI. Cloning sites, 5' end: SclI; 3' end: XhoI. Host: SOLR.

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Best Local Similarity	99.7%; Pred. No. 5.5e-132;
Matches 580; Conservative	0; Mismatches 2; Indels 0; Gaps 0

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Db	329	CCGCTGCACCAAGCCTATCGGGCTGCTGGAACGAGTTGAGACCCGTTTCGCCGAC	388
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RESULT	3						
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DEFINITION	AL157542	804 bp	mrna	linear	EST 24-FEB--2000		
ACCESSION	DKE276100816..r1.761 (synonym: hamy2)						
VERSION	DKE276100816.5', mRNA sequence.						
KEYWORDS	AL157542						
SOURCE	AL157542.1	GI:7057943					
ORGANISM	EST.						
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	Homo sapiens						
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						



[illegible]

RESULT	5	815 bp	mRNA	linear	EST 12-JAN-2001
BF785386					
LOCUS	BF785386				
DEFINITION	602111728F1 NCT-CGAP_K1d14 Mus musculus cDNA clone IMAGE:4239798				
	5', mRNA sequence.				

ACCESSION	Bf/85360	GI:12090422
VERSION	Bf/85386.1	
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	

ORGANISM Mus musculus; Chordata; Chariata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Rodentia; Sciurognathii; Muridae; Mus  
Mammalia; Eutelesta  
1 (bases 1 to 815)  
NIH-MGC help://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
JOURNAL  
TITLE  
COMMENT Contact: Robert Strausberg, Ph.D.  
mailto:robertstra@mail.nih.gov

FEATURES  
source

BASE COUNT	ORIGIN	SOURCE
166 a	212 c	296 g
		141 t
		Technology. Note: this is a NCI-CCAP Library. "
		Site. 2: Sali; Cloned unidirectionally. Primer: Oligo dr
		/note="Organ: kidney; Vector: pCMV_SPORT6; Site. 1: NotI;
		/lab_host="DH10B (T1 phage-resistant) "
		/clone_id="NCI-CCAP_Kid14 "
		/clone_image="4239798 "
		/db_xref="taxon:10090 "
		/strain="FVB/N"
		/organism="Mus musculus "

Query Match	76.5%	Score 445;	DB 10;	Length 815;
Best Local Similarity	96.5%	Pred. No. 3e-99;		
Matches 530;	Conservative	0;	Mismatches 10;	Indels 9;
				Gaps 7;

Db	2	CCGAGACACGGGCTTACTGTTGAC-TTGTAGGCTATAACCTGAGCAGACAGGTTA	60
QY	81	ttgtctgtggaacttgagcccttgggaagccagccgcgcgaccctgcacaaagccatgag	140
Db	61	TGTCTGTGGACTGTGGCCCTGGGAGAGCCCAACCCCGACCCGACCCGTCGACCAACGCAATGGC	120
QY	141	gactgtctggagaagagatttttagaccgcgtttccgcgcgaactctctgaaccttgcgcgtca	200
Db	121	GGCTGCTGGAAACGAG-TTGAGACCCGTTTCGCGCGACCTTGTCTGACTGCGCCCTCA	179
QY	201	gtatacgtgaccccaaggtcagcccaagcaagctcaaccaggttccgacgaacttt	260
Db	180	GCTTACACTGAACTCCAGGCTCAGCCCAACAGCGTTCCAGCGTTTCCAGCAACTTTT	239
QY	261	ccaagggagccctaacctggtggcgctctgtgacattcttgccttggaggtcgagcccttg	320
Db	240	CCAAAGGGGGCCCTTAACCTGGGGCCGCTGTGTGGCATTC---TGTCTTGGGGCTCCCTGTG	296
QY	321	tgctgagagtgccaacaagaanaatltgagacctltgtgtggacaagtgcagaatttgaaggt	380
Db	297	TGCTGAGATGTGTCAACAAGAAATGAGAGCC-TTGGTGGAGCAAGTCAGGATTTGATGTGT	355
QY	381	ggcctaccttgagaacaagctctgcgcgactggaatccacaagcaatgtgcgcttgagcgagtt	440
Db	356	GGCCTTACCTGGGAGACAGTGTGCTGACTGGAATCCACAGCACTGGGGGCTGGGGCGAATT	415
QY	441	caagagtcatacgggagcgaggcccttgagagaggaacagcgctctcgaggagggagactg	500
Db	416	CAGAAGCTTATACGGGGAGCGGGGCCCTTGAGAGAGGACAGG-GTCTGCGGAGAGGGACAC-G	473
QY	501	ggcatcaatgagaacagctgtgaacggggccgttgagactggggggcccttgataactgttag	560
Db	474	GGCATCAAGTAGAGACAGTGTGACGGGGGCGGTGGCACT-GGGGCCCTGTAACTGTTAGG	532
QY	561	ggacattttt 569	
Db	533	GGCCTTTT 541	

RESULT	6
B1770566	
LOCUS	B1770566
DEFINITION	60306036.F1 NIH_MGC_122 Homo sapiens CDNA clone IMAGE:5209862 5' mRNA sequence.

ACCESSION	BI//0386	GI:15762144
VERSION	BI770566.1	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	

ORGANISM  
Mammals  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 697)  
NHI-MGC <http://mgc.nhi.nih.gov/>  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Straussberg, Ph.D.  
[straussr@nhi.nih.gov](mailto:straussr@nhi.nih.gov)  
COMMENT

```
FEATURES
  source      Location/Qualifiers
1. 697
   /organism="Homo sapiens"
   /db_xref="taxon:9606"
   /clone="IMAGE:5209862"
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Host: SOLR  
Location/Qualifiers  
1. .854  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="MGD:MGI:1902183"  
/db\_xref="taxon:10090"  
/clone="2810435A13"  
/clone\_lib="RIKEN full-length enriched mouse cDNA library"  
/dev\_stage="10, 11 days embryo"  
196. .732  
/gene="Bcl2l2"  
196. .732  
/note="Bcl2-like 2"  
data source:MGD, source key:MGI:108052, evidence:ISS  
putative"  
/protein\_id="BAB28740.1"  
/db\_xref="GI:12850488"  
/translation="MAPPASPPDRALVADPVGYKLRQGYVCGAGPGEFADPLHQ  
AMKADDEFETFRFRTPSDLAOLHVPKSAOORPTQVDELFOGQPMGRVAFVYF  
GAALCAEYVKEPEPVGVDMMVAIETRLADMIHSSGWSVSSQLLSASLYKVG  
LHGKIGPLMGWGCAGRG"

BASE COUNT 178 a 229 c 264 g 183 t

Query Match 73.8% Score 429.8; DB 11; Length 854;  
Best Local Similarity 99.5% Pred. No. 1.7e-95;  
Matches 431; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 atgggaccccaagcctcaacccacagacacagcgtctagtgctgacttgtaagctat 60  
|||||  
196 ATGGGACCCCAAGCCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGAGGCTAT 255  
61 aggcctgaagcagaagggatgctgtgtgagctgcccctggggaagcccaagccgcagac 120  
|||||  
256 AAGCTGAGGCGAAGGGGTTATGCTGTGAGCTGGCCCTGGGGAAGGCCACGCCGCCGAC 315  
121 ccgctgacccaagcagcagctgctgctgagacagctlttgagaccglttcgcgcgacac 180  
|||||  
316 CCGCTGACCAAGCCATCGGGGCTGCTGAGACAGGATTGAGACCCGTTCCGCCGACAC 375  
181 ttctctgacctggccgctcagctacagctgaccccaagctgaagcccaagcagcttacc 240  
|||||  
376 TTCTGTGACCTGGCCGCTCAGCTACACGCTGACCCAGGCTCAGCCCAAGAGCTTCACC 435  
241 caagttccgaagaactttccaaggggcccctaactgagggcgctctgtgcaattctt 300  
|||||  
436 CAGGTTCCGAGCAACTTTCCAAAGGGGCCCTTAACCTGGGCCGCTTGTGCAATCTTT 495  
301 gtctttgggctgcccctgtgtgtcgtgagagtgctcaacaagaatgagagccttggtagga 360  
|||||  
496 GTCTTTGGGGCTGCCCTGTGCTGAGAGTGTCAACAAGAAATGAGACCTTTGGTGGGA 555  
361 caagtgcaagatgagatgtgtgtgctcactgagacagcttgcgtgactgagatcacagc 420  
|||||  
556 CAAGTGCAAGATGAGATGTGTGCTGAGAGACAGACGCTGCTGACATGGATGCACAGC 615  
421 agtggcggctggg 433  
|||||  
616 AGTGGGGCTGGG 628

RESULT 8  
BG298789 792 bp mRNA linear EST 21-FEB-2001  
LOCUS 602396527F1 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:4511215 5',  
DEFINITION mRNA sequence.  
ACCESSION BG298789  
VERSION BG298789.1 GI:13063794  
KEYWORDS EST.

SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 792)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov  
Tissue Procurement: The Cepko Laboratory  
cDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
plate: LLM10394 row: e column: 08  
High quality sequence stop: 713.

FEATURES  
source  
Location/Qualifiers  
1. .792  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4511215"  
/clone\_lib="NIH\_MGC\_94"  
/tissue\_type="retina"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: eye; Vector: pCMV-Sport6; Site: 1: NotI;  
Site: 2: SalI; Cloned unidirectionally; oligo-dT primed.  
Average insert size 3.3 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH-MGC library."

BASE COUNT 174 a 201 c 246 g 171 t

Query Match 71.6% Score 417; DB 10; Length 792;  
Best Local Similarity 98.6% Pred. No. 2.4e-92;  
Matches 431; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

1 atgggaccccaagcctcaacccacagacacagcgtctagtgctgacttgtaagctat 60  
|||||  
99 ATGGGACCCCAAGCCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGAGGCTAT 158  
61 aggcctgaagcagaagggatgctgtgtgagctgcccctggggaagcccaagccgcagac 120  
|||||  
159 AAGCTGAGGCGAAGGGGTTATGCTGTGAGCTGGCCCTGGGGAAGGCCACGCCGCCGAC 218  
121 ccgctgacccaagcagcagctgctgctgagacagctlttgagaccglttcgcgcgacac 180  
|||||  
219 CCGCTGACCAAGCCATCGGGGCTGCTGAGACAGGATTGAGACCCGTTCCGCCGACAC 278  
181 ttctctgacctggccgctcagctacagctgaccccaagctgaagcccaagcagcttacc 240  
|||||  
279 TTCTGTGACCTGGG-CGCTCAGCTACACGCTGACCCAGGCTCAGCCCAAGAGCTTCACC 337  
241 caagttccgaagaactttccaaggggcccctaactgagggcgctctgtgcaattctt 300  
|||||  
338 CAGGTTCCGAGCAACTTTCCAAAGGGGCCCTTAACCTGGGGCGCTTGTGCAATCTTT 397  
301 gtctttgggctgcccctgtgtgtcgtgagagtgctcaacaagaatgagagccttggtagga 360  
|||||  
398 GTCTTTGGGGCTGCCCTGTGCTGAGAGTGTCAACAAGAAATGAGACCTTTGGTGGGA 457  
361 caagtgcaagatgagatgtgtgtgctcactgagacagcttgcgtgactgagatcacagc 420  
|||||  
458 CAAGTGCAAGATGAGATGTGTGCTGAGAGACAGACGCTGCTGACATGGATGCACAGC 517  
421 agtggcggctggg 437  
|||||  
518 AGTGGGGCTGGGAAGA 534







RESULT 14  
 BG677345 749 bp mRNA 1linear EST 01-MAY-2001  
 LOCUS 602624059P1 NCI.CGAP.Skn4 Homo sapiens cDNA clone IMAGE:4748943 5',  
 DEFINITION mRNA sequence.  
 BG677345  
 ACCESSION BG677345.1 GI:13908742  
 VERSION EST.  
 KEYWORDS human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 749)  
 NIH-MGC <http://mgi.nci.nih.gov/>.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: James Cleaver, M.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 Cloning Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLM10601 row: f column: 16  
 High quality sequence stop: 732.

## FEATURES

source

1..749  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4748943"  
 /clone\_1ib="NCI.CGAP.Skn4"  
 /tissue\_type="squamous cell carcinoma"  
 /lab\_host="DH10B (p1 phage-resistant)"  
 /note="Organ: skin; Vector: PCMV-SPORE6; Site-1: NotI;  
 Site-2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.5kb. Library constructed by Life  
 Technologies. Note: this is a NCI-CGAP Library."

BASE COUNT 156 a 239 c 135 t  
 ORIGIN

Query Match 43.7%; Score 254.2; DB 10; Length 749;  
 Best Local Similarity 90.6%; Pred. No. 2.7e-52;

Matches 271; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 atggcagcccccagcctcaaccacacacagcggcctcgtgctgacttggtagctat 60  
 DB 126 ATGGCGACCCCGAGCTCGGCCCGACACACGGGCTGTGGGACACTTGTAGGTTAT 185  
 QY 61 agcttgagcagaaggtatgtctgtgagctgagccctggggaagccagccgagac 120  
 DB 186 AAGCTGAGAGCGAGAGGGTTATGTCTGTGAGAGCTGCCCGGGGAGGCCACAGAGCTGAC 245  
 QY 121 ccgctgagcagaagcattgctgctgctgagagagattgagaccgcttccgcccagac 180  
 DB 246 CCGCTGACACCAAGCCATGCGGGGAGCTGGAGATGATTCAGACCGCTTCGGGCGCAC 305  
 QY 181 ttcttgagcctgagcctcagctacagctgagcccaagctcagccagcaagcttacc 240  
 DB 306 TTCTCTGATCTGGCGGCTCAGCTGATGTGACCCAGGCTCAGCCCAACAAGCTTCAC 365  
 QY 241 caggttccgagcaacttcccaagggggccctactgagggccgtctgtgagcttct 299  
 DB 366 CAGGCTCTCCGATGACTTTTCAAGGGGGCCCAACTGAGGCGCCCTTGTAGCTTCTT 424

RESULT 15  
 BF204905 601 bp mRNA 1linear EST 06-NOV-2000  
 LOCUS BF204905  
 DEFINITION 601866718P1 NIH-MGC\_17 Homo sapiens cDNA clone IMAGE:4106836 5',

ACCESSION BF204905  
 VERSION BF204905.1 GI:11098491  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 601)  
 NIH-MGC <http://mgi.nci.nih.gov/>.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Cloning Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at: [image.llnl.gov](http://image.llnl.gov)  
 Plate: LLM987 row: d column: 05  
 High quality sequence stop: 561.

## FEATURES

source

1..601  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4106836"  
 /clone\_1ib="NIH-MGC\_17"  
 /tissue\_type="rhabdomyosarcoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: muscle; Vector: pORF6; Site-1: EcoRI;  
 Site-2: XhoI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
 for average insert size 1.8kb. Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using 2AP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 110 a 176 c 201 g 114 t  
 ORIGIN

Query Match 42.4%; Score 246.8; DB 10; Length 601;  
 Best Local Similarity 81.7%; Pred. No. 1.7e-50;

Matches 358; Conservative 0; Mismatches 72; Indels 8; Gaps 6;

QY 9 cccagcctcaaccag--acacagggcctcgtgagctgac-ttgtagctatagc 64  
 DB 164 CCCAGCTCGGCCCGACACACCGGCTGTGGGACACTTGTAGGTTAAGC 223  
 QY 65 tgaagcagaaggtatgtctgtgagctgagccctggggaagccagccgagccgc 124  
 DB 224 TGAGGAGAGAGGTTATGTCTGTGAGCTGGGCCCGGGAGGGGCCAGCAGCTGACCCAC 283  
 QY 125 tgcacaaagcattgctgctgagagagattgagacccgcttccgcg-caccttc 183  
 DB 284 TGCACCAAGCCAGCGCGGAGCTGGAGATGATTCAGACCGCTTCGCGCTCACCTTC 343  
 QY 184 tctgacctggcctcagct-acagctgaccccaagctcagccagcaagc-ctcacc 241  
 DB 344 TCTGATCTGGCGGCTCAGCTGATGTATCCAGGCTCAGCCCAACAAGCTTTCAC 403  
 QY 242 aggttccgagcaact-ttccaaagggccctcaactgggcccgtctgtgagctatc 300  
 DB 404 AGGTCTCCGTGTAAGCTTTTGAAGAAGGGGCCCAACTGGGGTTCCGTTGAGCTTCT 463  
 QY 301 gctttggagctgcccctgctgtgagagtgctcaacaagaatgagacclttgtgggga 360  
 DB 464 GTCTTGGGGCTGCACTGTGCTGAGAGTGTCAACAAGAGATGGAACCACTGAGGGA 523  
 QY 361 caagtcagagattgtagtggtgagcctacgtgagacagctgctgagctgagctcagcagc 420  
 DB 524 CAAATGAGAGAGTGAATGATGCTACTGTGAGACCGCGGTGTGCTGATCTGATCCAAAG 583

OY 421 agtggcggtggtggag 438  
|||  
Db 584 AGAGTGGGGTGTGTGGAG 601

Search completed: June 6, 2002, 11:24:34  
Job time: 5590 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 6, 2002, 11:58:14 ; Search time 1853.13 Seconds  
(without alignments)  
6572.256 Million cell updates/sec

Title: US-09-155-327E-8  
Perfect score: 582  
Sequence: 1 atggcgagccaccgacctcaac.....ccttttgcagcaagtga 582

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_scs:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_scs:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_hcg\_hum:\*  
31: em\_hcg\_inv:\*  
32: em\_hcg\_other:\*  
33: em\_hcg\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Match	Length	DB ID	Description
------------	-------------	--------	-------	-------------

1	578.8	99.5	582	10	MMU59746	US9746 Mus musculus
2	578.8	99.5	3476	10	AF030769	AF030769 Mus muscu
3	563.4	96.8	581	6	AX022531	AX022531 Sequence
4	563.4	96.8	581	6	AX030819	AX030819 Sequence
5	562.8	96.7	582	10	AF096291	AF096291 Rattus no
6	558.2	95.9	579	6	AR020779	AR020779 Sequence
7	524.4	90.1	582	9	HS059747	US9747 Human Bcl-w
8	521.2	89.6	3542	9	D87461	D87461 Human mRNA
9	519.6	89.3	583	6	AX022529	AX022529 Sequence
10	519.6	89.3	583	6	AX030817	AX030817 Sequence
11	519.6	89.3	1437	9	BC021198	BC021198 Homo sapi
12	515	88.5	579	6	AR020780	AR020780 Sequence
13	405.6	69.7	151212	2	AC079885	AC079885 Rattus no
14	405.6	69.7	181282	2	AC084240	AC084240 Rattus no
15	372.2	64.0	196292	2	CNS0000B	AL049829 Human chr
16	241.2	41.4	749	5	XR1	X82462 X.laavis R1
17	218.6	37.6	6049	5	AX345130	AX345130 Sequence
18	192.6	33.1	6049	6	AX345131	AX345131 Sequence
19	142.4	24.5	1252	4	AB073983	AB073983 Canis fam
20	140.8	24.2	702	4	AY005131	AY005131 Oryctolag
21	139.2	23.9	766	4	AF164517	AF164517 Ovis arie
22	137.6	23.6	541	4	AF245488	AF245488 Bos tauru
23	136	23.4	541	4	AF245487	AF245487 Bos tauru
24	136	23.4	541	4	AF245489	AF245489 Bos tauru
25	135	23.2	764	10	RN010579	U10579 Rattus norv
26	135	23.2	1742	6	BD006625	BD006625 A mutagen
27	135	23.2	1742	10	RN072350	U72350 Rattus norv
28	135	23.2	2232	10	RNCBLXLS	X82537 R.norvegicu
29	134.6	23.1	926	6	AR054021	AR054021 Sequence
30	134.6	23.1	926	6	AR118504	AR118504 Sequence
31	134.6	23.1	926	6	AR124952	AR124952 Sequence
32	134.6	23.1	926	6	AR144311	AR144311 Sequence
33	134.6	23.1	926	6	AR172594	AR172594 Sequence
34	134.6	23.1	926	6	E58777	E58777 Screening m
35	134.6	23.1	926	6	I52011	I52011 Sequence 5
36	134.6	23.1	926	9	HSBCLXL	223115 H.sapiens b
37	134.6	23.1	1236	9	AX085490	AX085490 Sequence
38	134.6	23.1	2575	9	BC019307	BC019307 Homo sapi
39	134.6	23.1	7372	6	E23357	E23357 Virus vecto
40	134.2	23.1	720	4	AF216205	AF216205 Sus scrof
41	134.2	23.1	752	4	SSJ001203	AJ001203 Sus scrof
42	133.4	22.9	1184	5	GGU26645	U26645 Gallus gall
43	131.2	22.5	1455	6	AX085496	AX085496 Sequence
44	130.2	22.4	726	10	RN034963	U34963 Rattus norv
45	130.2	22.4	726	10	S76513	S76513 bcl-x-aapt

## ALIGNMENTS

RESULT 1  
LOCUS MMU59746 582 bp mRNA linear ROD 29-SEP-1996  
DEFINITION Mus musculus Bcl-w (bcl-w) mRNA, complete cds.  
ACCESSION U59746  
VERSION U59746.1 GI:1572494

## KEYWORDS

## SOURCE

house mouse.  
Mus musculus

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 582)

Gibson, L., Holmgren, S.P., Huang, D.C., Bernard, O., Copeland, N.G.,  
Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S.,  
bcl-w, a novel member of the bcl-2 family, promotes cell survival  
Oncogene 13 (4), 665-675 (1996)

96358615

2 (bases 1 to 582)

Gibson, L., Holmgren, S.P., Huang, D.C.S., Bernard, O., Adams, J.M. and  
Cory, S.,  
Direct Submission  
Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and  
Eliza Hall Institute of Medical Research, PO Royal Melbourne

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES  
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 Hospital, Parkville, Victoria 3050, Australia  
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 Db 421 AGTGGGAGCTGGGCGGAGTTCACAGCTTATACGGGAGCGGCGCTTGGAGGAGCAGG 480  
 QY 481 cgtctcggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 540  
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RESULT 2  
 AF030769 3476 bp mRNA linear ROD 16-NOV-1997  
 LOCUS AF030769  
 DEFINITION Mus musculus BCL-W (Bcl-w) mRNA, complete cds.

ACCESSION AF030769  
 VERSION AF030769.1 GI:2623249  
 KEYWORDS  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 3476)  
 Ross, A.J., Waymire, K.G., Moss, J.E., Parlow, A.F., Russell, L.D. and  
 Macgregor, G.R.  
 Bcl-w is required for testis homeostasis  
 Unpublished  
 2 (bases 1 to 3476)  
 Ross, A.J. and Macgregor, G.R.  
 Direct Submission  
 Submitted (21-OCT-1997) Center for Molecular Medicine, Emory  
 University, 1462 Clifton Road, Atlanta, GA 30322, USA  
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Matches 580; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 QY 121 ccgctgac 180  
 Db 299 CCGCTGAC 358



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Db	479	GTCCTTGGGCGCTGCCCTGTGTGCTGAGAGTCTCAACAAAGAAAGGAGCCTTTGTGTGGGA	538
QY	361	caagtgcaagatgttatgtgtgtgtcctaactgagacagctcgtcgtactgtgatccacagc	420
Db	539	CAAGTGCAGGATGTGATGTGTGCTTACCTTGAGACACAGCTCTGGCTGACTGATCCACACAGC	598
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Db	599	AGTGGGGGCTGGGGGAGATTCCAGCTCTATACGGGGACGGGGCCCTGGAGAGGACACGG	658
QY	481	cgtctcgaggaggggaacttggcatcagtgtagaggaagtcgtcgaacgggggcccgttgacatg	540
Db	659	CGTCTCGGGGAGGGGGAACGTGGGCACATGTGAGGAGAGTGCATGACGGGGGCCGTGGCACTG	718
QY	541	ggggcccttgtaactgtataggggccctttttctagacaagtta	582
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DEFINITION	Sequence 8 from Patent EP0932674.				
ACCESSION	AX022531				
VERSION	AX022531.1	GI:10046127			
KEYWORDS					
SOURCE	unidentified.				
ORGANISM	unidentified.				
REFERENCE	1 (bases 1 to 581)				
AUTHORS	Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.				
TITLE	A novel mammalian gene, bcl-2, belongs to the bcl-2 family of apoptosis-controling genes				
JOURNAL	Patent: EP 0932674-A 8 04-AUG-1999;				
FEATURES	AMRAD OPERATIONS PTY LTD (AU)				
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SOURCE	unidentified.				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 581)				
AUTHORS	Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.				
TITLE	A novel mammalian gene, bcl-w, belongs to the bcl-2 family of apoptosis-controlling genes				
JOURNAL	Patent: WO 9735971-A 8 02-OCT-1997;				
	ADAMS JERRY MCKEE (AU) ; HOLMGREEN SHAUN P (AU) ; CORY SUZANNE (AU)				
	; GIBSON LEONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)				
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ACCESSION AF096291
VERSION   AF096291.1 GI:3747129
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           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
           Rattus.
REFERENCE 1 (bases 1 to 582)
AUTHORS   Hamner,S., Skoglosa,Y. and Lindholm,D.
TITLE     Differential expression of bcl-w and bcl-x messenger RNA in the
           developing and adult rat nervous system
JOURNAL   Neuroscience 91 (2), 673-684 (1999)
MEDLINE   99292146
PUBMED    10366024
REFERENCE 2 (bases 1 to 582)
AUTHORS   Hamner,S., Skoglosa,Y. and Lindholm,D.
TITLE     Direct Submission
JOURNAL   Submitted (01-OCT-1998) Developmental Neuroscience, Uppsala
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LOCUS   AR020779 579 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 1 from patent US 5789201.
ACCESSION AR020779
VERSION   AR020779.1 GI:3975394
KEYWORDS
SOURCE    Unknown.
           Unclassified.
ORGANISM   Unknown.
REFERENCE 1 (bases 1 to 579)
AUTHORS   Guastella,J.
TITLE     Genes coding for bcl-y a bcl-2 homologue

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DB7461 LOCUS 3542 bp mRNA linear PRI 06-OCT-2001  
 DEFINITION Human mRNA for KIAA0271 gene, complete cds.  
 ACCESSION DB7461  
 VERSION DB7461.1 GI:1944417  
 KEYWORDS KIAA0271.  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE Nagase,T., Seki,N., Ishikawa,K., Ohira,M., Kawarabayashi,Y.,  
 Ohara,O., Tanaka,A., Kotani,H., Miyajima,N. and Nomura,N.  
 Prediction of the coding sequences of unidentified human genes. VI.  
 The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by  
 analysis of cDNA clones from cell line KG-1 and brain  
 DNA Res. 3 (5), 321-329 (1996)  
 JOURNAL 97191544  
 MEDLINE 2 (bases 1 to 3542)  
 AUTHORS Ohara,O., Nagase,T., Kikuno,R. and Nomura,N.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-AUG-1996) Osamu Ohara, Kazusa DNA Research Institute;  
 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan  
 (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)  
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 DB 657 CGTCTGGCGGAGGGGAACCTGGGCATCATGAGACAGATGCTGACGGGGCCGTGGCACTG 716  
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 LOCUS AX022529  
 DEFINITION Sequence 6 from Patent EP0932674.  
 ACCESSION AX022529  
 VERSION AX022529.1 GI:10046125  
 KEYWORDS  
 SOURCE unidentified.  
 ORGANISM unidentified.  
 REFERENCE 1 (bases 1 to 583)  
 AUTHORS Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.  
 TITLE A novel mammalian gene, bcl-w, belongs to the bcl-2 family of  
 apoptosis-controlling genes  
 JOURNAL Patent: EP 0932674-A 6 04-AUG-1999;  
 AMRAD OPERATIONS PTY LTD (AU)  
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 source Location/Qualifiers  
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 BASE COUNT 105 a 157 c 210 g 111 t  
 ORIGIN  
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 Best Local Similarity 93.3%; Pred. No. 4e-111;  
 Matches 543; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

OY	181	tctctgacactggcgcgtcagctacacgcygaccccaagggctcgaagcccaagccttcacc	240
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OY	241	caagttccgaagaaactttccaagggggccctaactgaggccgctctgtgcatcttt	300
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OY	301	gtctctggagctgcccctgtgctgagagtgctcaacaaagaatgagccctttgtgtgga	360
Db	301	CTCTTTGGGCGCTGCAGCTGTGCTGACAGTCTCAACAAGAGATGAGAACCACTGTGGGA	360
OY	361	caagtgcaggaattgattggtgctgactcctgagagacaagctgctgactgattccacagc	420
Db	361	CAAGTCAGGAGTGATGTGTGTCCTACTTGGAGACGGGGCTGGTGCAGCTGATCCACAGC	420
OY	421	agtgccgactggggcgagttcacagctctatacggggaacggggccctggaggaagcagcg	480
Db	421	AGTGGGGGCTGGCGGAGTTCAAGACTTAAACGGGGACGGGGCCCTGGAGAGGCGGG	480
OY	481	cgctgcgggaggggaactggtgcatcaatgagggaacagtgcgcgaacgggggcccgtggcactg	540
Db	481	CCTTCGCGGAGGGAACCTGGGCATCACTGAGACAGTCTGACGCGGGCGCTGGCACTG	540
OY	541	ggggccctgtaactgtatagggccttttltgctaagaatga	582
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LOCUS	AX030817	583 bp	
DEFINITION	Sequence 6 from Patent WO9735971.		
ACCESSION	AX030817		
VERSION	AX030817.1	GI:10276311	

SOURCE	ORGANISM	REFERENCE	TITLE	JOURNAL	FEATURES
source	unidentified.	1 (bases 1 to 583)	Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.		
	unidentified		A novel mammalian gene, bcl-w, belongs to the bcl-2 family of		
	unclassified.		apoptosis-controlling genes		
		Patent: WO 9735971-A 6 02-OCT-1997;			
		ADAMS JERRY MCKEE (AU) ; HOLMGREEN SHAUN P (AU) ; CORY SUZANNE (AU)			
		; GIBSON LIONTE M (AU) ; AMPAD OPERATIONS Pty LTD (AU)			
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	111 t	

Query Match	80.3%	Score 519.6	DB 6	Length 583
Best Local Similarity	93.3%	Pred. No. 4e-111		
Matches 543	Conservative	0	Mismatches 39	Indels 0
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Qy	61 aggcctagagcaagaaggttatgtctgtgtgagctgtgaccttgagggaagcccgagccgac	120		

Db	61	AAGCTGAGCGAAGAGGTTATGCTGTGGAGACGTGGCCCCGGGGGAGGGCCACAGCTGCAC	120
Oy	121	ccgcgtcaccaagccatgctgcggctgctgtgagacagagttttaagaccgcttcgcgcgcacc	180
Db	121	CGCGTGCACCAAGCCATCCGGCAGCTGGAGATGATAGTTTCAGACCCGCTTCGGCGCAC	180
Oy	181	ttctctgacccggccgcctcagctacgtacgtaccccaagctcagcccgacaagcttcacc	240
Db	181	TTCTCTGATCTGGCGGCTTCAGCTGCATGTGACCCACAGGCTCAGCCCGACAAGCTTTCACC	240
Oy	241	caagcttccgcagcaactttccaaaggggcccctaacctggggcgctctgtggcacttc	300
Db	241	CAGGCTCTCGAAGAACTTTTTCAGGGGGGCCCAACTGCGGCCCTTGTAGCCTTCTTT	300
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Db	301	CTCTTTGGGGCTGCACCTGTGTCTAGAGTGCACACAGAGAGATGGAACCACTGGTGSGGA	360
Oy	361	caagtcaggaattgtagtgtgtgccttaacttggagagacacttgcgtgcagctgattccaaagc	420
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Db	421	AGTGGGGGCTGGGGGGAAGTTCAACAGCTTATACGGGGACGGGGCCCTGGAGAGGGCGGG	480
Oy	481	cgctctgcggaggggaactgggcatcaatcgtgaagaaagatgtctaacgggggcccgtgcactg	540
Db	481	CGCTCTGGGAGGGGAACCTGGCATCAGTGAAGACAGTCTACCGGGGGCCGTGGCACAG	540
Oy	541	ggggccctgttaactgttaaggcccttcttgtctagcaagtga	582
Db	541	GGGGCCCTGTGTACTGTAGGGCCCTTTTGTGTCAGCAAGTGA	582

RESULT	11
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LOCUS	1437 bp mRNA linear PRI 22-JAN-2002
DEFINITION	Homo sapiens, BCL2-like 2, clone MGC:10675 IMAGE:3944307, mRNA,
ACCESSION	BC021198 complete cds.
VERSION	BC021198
KEYWORDS	BC021198.1 GI:18203706
SOURCE	MGC.
ORGANISM	human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1437) Strausberg,R. Direct Submission Submitted (14-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	

REMARK	COMMENT
<p>NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>            Contact: MGC help desk            Email: <a href="mailto:cgabbs-remail.nih.gov">cgabbs-remail.nih.gov</a>            Tissue Procurement: DCDT/DTP            CDNA Library Preparation: Rubin Laboratory            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)            DNA Sequencing By: National Institutes of Health Intramural            Sequencing Center (NISC),            Gaithersburg, Maryland,            Web site: <a href="http://www.nisc.nih.gov/">http://www.nisc.nih.gov/</a>            Contact: <a href="mailto:nisc.mgc@nih.gov">nisc.mgc@nih.gov</a>            nisc.mgc@nih.gov</p>	<p>Sherchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,            Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.            Dierlich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.            Lim, M., Maduro, O.L., Mastello, C., Mastrian, S.D., McCloskey, J.C.,            McDowell, J., Pearson, R., Snyder, B., Stantirpop, S., Thomas, P.J.,            Tlionson, E.E., Touchman, J.W., Tsungueon, C., Vogt, J.L., Walker, M.A.,            Zhang, L.-H. and Green, E.D.</p>

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.livl.gov>  
 Series: IRAL Plate: 15 Row: k Column: 19  
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14574571.  
 Location/Qualifiers

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## CDS

BASE COUNT 303 a 509 g 282 t  
 ORIGIN

Query Match 89.3%; Score 519.6; DB 9; Length 1437;  
 Best Local Similarity 93.3%; Pred. No. 3.6e-111;

Matches 543; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

1 atggagacccagcctcaacccacagacacagggctctagtgctgacttctgtagctat 60  
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 61 aggcctgagcagaagggatgtctgtgagctggccctggaggaagggccgcgcgcag 120  
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## RESULT 12

AR020780

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

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## RESULT 13

AC079885

LOCUS

DEFINITION

ACCESSION

VERSION

AC079885 151212 bp DNA linear HTG 08-NOV-2000  
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 Norway, WORKING DRAFT SEQUENCE, 5 unordered pieces.





TITLE Vogt, J.L., Walker, M.A., Wetherby, K.D. and Green, E.D.  
 JOURNAL NISC Mouse Sequencing Initiative  
 REFERENCE Unpublished  
 AUTHORS 2 (bases 1 to 181282)  
 TITLE Green, E.D.  
 JOURNAL Direct Submission  
 COMMENT Submitted (18-OCT-2000) NIH Intramural Sequencing Center, 8717  
 Genomex Center  
 Center: NIH Intramural Sequencing Center  
 Center code: NISC  
 Web site: http://www.nisc.nih.gov  
 Contact: nisc\_mouse@nih.gov  
 Project Information  
 Center project name: r1  
 Center clone name: 103L21

----- Summary Statistics -----  
 Sequencing vector: plasmid; n/a; 100% of reads  
 Chemistry: dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 179798 bases at least Q40  
 Consensus quality: 180132 bases at least Q30  
 Consensus quality: 180274 bases at least Q20  
 Insert size: 138000; agarose-gel  
 Insert size: 160000; pulse-field-gel  
 Quality coverage: 15.02x in Q20 bases; agarose-gel  
 Quality coverage: 12.95x in Q20 bases; pulse-field-gel  
 Quality coverage: 11.45x in Q20 bases; sum-of-coverage

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 4 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

\* 1 5430: contig of 5430 bp in length  
 \* 5431 5530: gap of unknown length  
 \* 5531 39503: contig of 33973 bp in length  
 \* 39504 39603: gap of unknown length  
 \* 39604 85797: contig of 46189 bp in length  
 \* 85793 85892: gap of unknown length  
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 Location/Qualifiers

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 Best Local Similarity 86.6%; Pred. No. 8.6e-85;  
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 DEFINITION from chromosome 14 of Homo sapiens (human), complete sequence.  
 ACCESSION AL049829  
 VERSION AL049829.4 GI:8217859  
 KEYWORDS HTG.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 196292)  
 AUTHORS Heilig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P.,  
 Brothier, P., Catolico, L., Barbe, V., Pelletier, E., Artiguenave, F.,  
 Levy, M., Eckenberg, R., Bruls, T., deBardis, V., Crnaud, C.,  
 Gysay, G., Saurin, W. and Weissenbach, J.  
 Sequencing of the human chromosome 14  
 Unpublished  
 2 (bases 1 to 196292)  
 Genoscope.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-MAY-2001) Genoscope - Centre National de Sequencage :  
 BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 COMMENT On Jun 3, 2000 this sequence version replaced gi:6138746.  
 ----- Genome Center  
 Center: Genoscope / Centre National de Sequencage  
 Center code: GS  
 Web site: http://www.genoscope.cns.fr/  
 Contact: seqref@genoscope.cns.fr  
 The following BAC sequence is oriented from the r7 to the sp6 end.  
 Upstream BAC (overlapping the r7 end) : R-244K17  
 Downstream BAC (overlapping the sp6 end) : C-2201G16 (AC-AL132855)  
 ----- Summary Statistics -----





Thu Jun 6 16:39:24 2002

us-09-155-327e-8.rge

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Page 12



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DB 541 GGGGCCCTGTAACTGAGGGGCTTTTGTCTAGCAAG 579

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# RESULT 2

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US-08-978-523-2
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; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540

```

```

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-08-978-523-2

```

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Query Match 98.2%; Score 572.6; DB 2; Length 579;
Best Local Similarity 99.3%; Pred. No. 1,8e-140;
Matches 575; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 1 atggcagccacgctcggcccaagacacagggctctggtgcaagactttagtatt 60
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QY 61 aagctgagcagaagggtatgtctgtgagctgcccgggagggcccaagagctgac 120
DB 61 AAGCTGAGCAGAGGTTATGTCGTGAGCTGGGCCGGGGAGGGCCACAGCTGAC 120
QY 121 ccgttcacacaaagcattgcgggcaagctgagatgagttcgaagccgcttcggcgacc 180
DB 121 CCAGTGCACCAAGCCATGGCGGACGCTGAGATGAGATGAGACCCGCTTCGGCGCAC 180
QY 181 ttctcgtatctgagcgtcaagctgcatgtgaccccaaggtcagccagaagcttaacc 240
DB 181 TTCTCGATCTGGCGGCTGACGTGCTGAGAGTGAACAAGAGATGGAACCACTGGTGGGA 240
QY 241 caggttcacgaagcattttcaaggggcccaactggggccgctttagcctctt 300
DB 241 CAGGTCCTCCAGTGAATTTTCAAGGGGCCCCCACTGGGGCCGCTTGACTTCTTT 300
QY 301 gtcttggggcgtcactgtgtctgagagtgatcaacaaggagatggaacacatgttggga 360
DB 301 GTCTTTGGGGCTGCACTGTGTCTGAGAGTGAACAAGAGATGGAACCACTGGTGGGA 360
QY 361 caagtgcaagagtgatggtgagcctacacgtgagacgagcgtgctgactggtccacagc 420
DB 361 CAAGTGCAGAGTGAATGTTGTCCTACCTGAGAGCGGCGCTGCTGACTGATCCACAGC 420
QY 421 agtgggggctggcgaggttcacagctctatacggggagcgggcccctggagagggcgcg 480
DB 421 AGTGGGGGCTGGCGGAGTTCACAGCTCTATACGGGGAGCGGGCCCTGGAGAGCGCGG 480
QY 481 cgtctcgaggaaggaggaactgagtcacagtgaggaagacatgctgagcggcgctgacatg 540
DB 481 CGTCTGCGGAGGAGGAGTGGGCTACATGAGAGACAGTGTGACGGGGCGGCTGACATG 540
QY 541 ggggcccctgtaactgttaggggcttttctgtagcaag 579
DB 541 GGGGCCCTGTAACTGAGGGGCTTTTGTCTAGCAAG 579

```

## RESULT 3

```

US-08-798-897-1
; Sequence 1, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/798,897  
 FILING DATE: February 11, 1997  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Esmond, Robert W.  
 REGISTRATION NUMBER: 32,893  
 REFERENCE/DOCKET NUMBER: 1483.0140001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-2600  
 TELEFAX: 202-371-2540  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 579 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: both  
 MOLECULE TYPE: cDNA  
 US-08-798-897-1

Query Match 90.5%; Score 527.8; DB 1; Length 579;  
 Best Local Similarity 94.5%; Pred. No. 8.5e-129;  
 Matches 547; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 1 atggagaccacagctcgcgccccagagacacagggctctgtgtgagagactttaggtat 60  
 Db 1 ATGGAGACCCAGCCTCAACCCAGACACGCGGCTCTGTAGTGTAGTGTAGTGTAGT 60  
 QY 61 aagcttgagcagaaggtatgtctgtgagctggtcccgaggagggcccaagctgac 120  
 Db 61 AAGCTGAGACAGAGGTTATGTCTGTGTGAGCTGCGCTGGGAGAGCCACAGCGCGAC 120  
 QY 121 cccgtgacacaaagcctgagggagctgagatgagttgagagcccgcttcggcgagcc 180  
 Db 121 CCGCTGACACAAAGCCTGAGGGAGCTGAGAGAGAGTTGAGACCGCTTCCGCGCCAGC 180  
 QY 181 ttctctgactgagctcagctcagctgcatgtgacccagagctcagccagagacgttacc 240  
 Db 181 TTCTCTGACCTGCGGCTCAGCTACGTACGTACGCCAGAGCTCAGCCAGACCGCTTACCC 240  
 QY 241 caagtcacagcagaacttttcaagggggcccaagctggggcgctgtgtgagcttctt 300  
 Db 241 CAGGTTCCGACGAACTTTTCCAAAGGGGGCCCAACTGGGGCGCTGTGTGAGCTTCTTT 300  
 QY 301 gctcttgagggctgacgtgtgtcgtgagagtgctcaacaaagaaatgagccattgtggga 360  
 Db 301 GCTCTTGGGGCTGCGCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGCCATTGTGGGA 360  
 QY 361 caagtcagagagtgatgtgtgagctcagctgagagcggcgctgtgtgtgtgtgtgtgt 420  
 Db 361 CAAGTCAGAGATGTGATGTGATGTGATGTGAGACAGCGCTGTGTGTGTGTGTGTGTGT 420  
 QY 421 aatggagggctgagggaggttcaacagctctatacagggagggcgccctggagagggcg 480  
 Db 421 AATGGAGGCTGAGGGAGGTTCAACAGCTCTATACGGGAGGGGCGCCCTGGAGAGGCGAG 480  
 QY 481 cgtctcagagagggagaaacttgagcatcaatgagagagtgctgagagggggcggtgac 540  
 Db 481 CGTCTCAGAGAGGGAGAACTTGAAGCATCACTGAGAGACAGTGTGAGAGGGGCGGTGAC 540  
 QY 541 ggggagggctgagggagggcgctttttgtgagcaag 579  
 Db 541 GGGGAGGGCTGAGGGAGGGCGCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 579

RESULT 4  
 US-08-978-523-1  
 Sequence 1, Application US/08978523  
 Patent No. 5883229

GENERAL INFORMATION:  
 APPLICANT: Guastella, John  
 TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2  
 TITLE OF INVENTION: Homologue  
 NUMBER OF SEQUENCES: 53  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 STREET: 1100 New York Avenue, N.W., Suite 600  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/978,523  
 FILING DATE: herewith  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/798,897  
 FILING DATE: February 11, 1997  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Esmond, Robert W.  
 REGISTRATION NUMBER: 32,893  
 REFERENCE/DOCKET NUMBER: 1483.0140002  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-2600  
 TELEFAX: 202-371-2540  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 579 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: both  
 MOLECULE TYPE: cDNA  
 US-08-978-523-1

Query Match 90.5%; Score 527.8; DB 2; Length 579;  
 Best Local Similarity 94.5%; Pred. No. 8.5e-129;  
 Matches 547; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 1 atggagaccacagctcgcgccccagagacacagggctctgtgtgagagactttaggtat 60  
 Db 1 ATGGAGACCCAGCCTCAACCCAGACACGCGGCTCTGTAGTGTAGTGTAGTGTAGT 60  
 QY 61 aagcttgagcagaaggtatgtctgtgagctggtcccgaggagggcccaagctgac 120  
 Db 61 AAGCTGAGACAGAGGTTATGTCTGTGTGAGCTGCGCTGGGAGAGGCCACAGCGCGAC 120  
 QY 121 cccgtgacacaaagcctgagggagctgagatgagttcagagccgcttcggcgagcc 180  
 Db 121 CCGCTGACACAAAGCCTGAGGGAGCTGAGAGACAGATTGAGACCCCTTCCGCGCACCC 180  
 QY 181 ttctctgactgagctcagctcagctgcatgtgacccagagctcagccagagacgttacc 240  
 Db 181 TTCTCTGACCTGCGCTCAGCTACGTACGTACCCAGAGCTTAGCCCTTCCGCGCACCC 240  
 QY 241 caagtcacagcagaacttttcaagggggcccaacttgaggcgccgtgtgtgtgtgtgtgt 300  
 Db 241 CAGGTTCCGACGAACTTTTCCAAAGGGGGCCCAACTGGGGCGCTGTGTGAGCTTCTTT 300  
 QY 301 gctcttgagggctgacgtgtgtcgtgagagtgctcaacaaagagagatggagacactgtgga 360  
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 QY 361 caagtcagagagtgatgtgtgagctcagctgagagcggcgctgtgtgtgtgtgtgtgtgt 420  
 Db 361 CAAGTCAGAGATGTGATGTGATGTGATGTGAGACAGCGCTGTGTGTGTGTGTGTGTGT 420

OY	421	agcggggggttcgggcgggaattcaacagccctatacgggacggggccctcgtgagagcgcg	480
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OY	481	cgctcgcggaggggaactcgggacatacgatgagacagctcctaacggggccgtgcacatg	540
Db	481	CGCTCTCGGGAGGGGAACTGGGCACTACGTAGTAAAGCAAGTCTCAACGGGGCGCTGGCACTG	540
OY	541	ggggccctcgttactcgtataggggcccttttctgtagaag	579
Db	541	GGGGCCCTGTACTGTATAGGGCCCTTTTCTGTAGCAAG	579

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1  RESULT 5
2  US-08-081-448-5
3  ; Sequence 5, Application US/08081448
4  ; Patent No. 5646008
5  ;
6  ; GENERAL INFORMATION:
7  ; APPLICANT: Thompson, Craig B.
8  ; APPLICANT: Boise, Lawrence H.
9  ; TITLE OF INVENTION: Vertebrate Apoptosis Gene:
10 ; TITLE OF INVENTION: Compositions and Methods
11 ; NUMBER OF SEQUENCES: 8
12 ; CORRESPONDENCE ADDRESS:
13 ; ADDRESSEE: Arnold, White & Durkee
14 ; STREET: 321 No. 5646008th Clark Street, Suite 800
15 ; CITY: Chicago
16 ; STATE: IL
17 ; COUNTRY: USA
18 ; ZIP: 60610
19 ;
20 ; COMPUTER READABLE FORM:
21 ; MEDIUM TYPE: Floppy disk
22 ; COMPUTER: IBM PC compatible
23 ; OPERATING SYSTEM: PC-DOS/MS-DOS
24 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
25 ; CURRENT APPLICATION DATA:
26 ; APPLICATION NUMBER: US/08/081,448
27 ; FILING DATE: 19930622
28 ;
29 ; CLASSIFICATION: 424
30 ;
31 ; ATTORNEY/AGENT INFORMATION:
32 ; NAME: No. 5646008thrup, Thomas E.
33 ; REGISTRATION NUMBER: 33,268
34 ; REFERENCE/DOCKET NUMBER: ARCD090
35 ; TELECOMMUNICATION INFORMATION:
36 ; TELEPHONE: 312-744-0090
37 ; TELEFAX: 312-755-4489
38 ;
39 ; INFORMATION FOR SEQ ID NO: 5:
40 ; SEQUENCE CHARACTERISTICS:
41 ; LENGTH: 926 base pairs
42 ; TYPE: nucleic acid
43 ; STRANDEDNESS: single
44 ; TOPOLOGY: linear
45 ;
46 ; MOLECULE TYPE: DNA (genomic)
47 ; FEATURE:
48 ;
49 ; NAME/KEY: CDS
50 ; LOCATION: 135..836
51 ;
52 ; US-08-081-448-5

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	Query Match	22.5%	Score 131,	DB 1,	Length 926;	
	Best Local Similarity	56.3%	Pred. No.	2.2e-25;		
	Matches 245; Conservative	0;	Mismatches 190;	Indels 0;	Gaps 0;	
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Dd	364	ccccggagtgatgcccatctgcagcagctaaaccaagcccttaggaagaagcagcacagc	423			
OY	158	tctgagaccgcttcctggcgcaaccttctctgatctctgctgcgcacatcatgatgtaaccaa	217			
Dd	424	tttgaaactgcgcgttaccgcgcggcatctcagtaagcaactgcatactccactctccattacccca	483			
OY	218	gtctaacgccgcgaagccttcaccacgagtctctcgacgaactcttttcaaggaggccccaact	277			

Db	484	GGACGCAATTCAGACCTTTGAACACAGTATGCAATCACTCTCCGGATGGGGTAAACT	54.3
QY	278	ggggcgccctttagcctctcttcttcttcttggcgctgcactgtgtctgaagtgatcaaca	33.7
Db	544	GGGGTCCATTGTGGCGCTTTCTCTCTCCGCGGGGCACTGTGCGTGGAAACCTAAGCA	60.3
QY	338	aggagatggaaccacacgtggtgggaacaagtgacgaagtgatagtgtgcctactgtgaagc	39.7
Db	604	AGGAGATGCCAGGTATTGGTGGATCGGATCGCAGCTTGATGGAGGCCACTTACCTGATATACCC	65.3
QY	398	ggtctgctgactgataccacacgaatgtggggctctggcgagatccaaactctataagggg	45.7
Db	664	ACCTAGAGCCTTGATGCCAGGAAAGCGCGCGCTGCGATCTTTTGTGCAACTCTATGGGA	72.3
QY	458	accggggcccttgagaggaagcgcgcgctctgcgggaagggaacttgggcatacagtgagacag	51.7
Db	724	ACAATGCAAGACGCGCAGAGACCGAAGAGGCGACGAAACGCTTCAACCGCTGTGTTCCGTACGG	78.3
QY	518	tgctgaagggggcgcg	53.2
Db	784	GCATGACTGTGGCGG	79.8

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1      RESULT 6
2      US-08-470-670A-6
3      ; Sequence 6, Application US/08470670A
4      ; Patent No. 5834309
5      ; Patent No. 5834309 5710045
6      ;
7      ; GENERAL INFORMATION:
8      ; APPLICANT: Thompson, Craig B. B.
9      ; APPLICANT: Boise, Lawrence H.
10     ; TITLE OF INVENTION: VENTERATE APOPTOSIS GENE:
11     ; TITLE OF INVENTION: COMPOSITIONS AND METHODS
12     ; NUMBER OF SEQUENCES: 18
13     ;
14     ; CORRESPONDENCE ADDRESSES:
15     ; ADDRESSEE: Arnold, White & Durkee
16     ; STREET: P. O. Box 4433
17     ; CITY: Houston
18     ; STATE: Texas
19     ; COUNTRY: United States of America
20     ; ZIP: 77210
21     ;
22     ; COMPUTER READABLE FORM:
23     ; MEDIUM TYPE: Floppy disk
24     ; COMPUTER: IBM PC compatible
25     ; OPERATING SYSTEM: PC-DOS/MS-DOS
26     ; SOFTWARE: PatentIn Release #1.0, Version #1.30
27     ;
28     ; CURRENT APPLICATION DATA:
29     ; APPLICATION NUMBER: US/08/470,670A
30     ; FILING DATE:
31     ; CLASSIFICATION: 514
32     ; PRIOR APPLICATION DATA:
33     ; APPLICATION NUMBER: US 08/081,448
34     ; FILING DATE: 22-JUN-1993
35     ; ATTORNEY/AGENT INFORMATION:
36     ; NAME: Highlander, Steven L.
37     ; REGISTRATION NUMBER: 37,642
38     ; REFERENCE/DOCKET NUMBER: ARCD:090--1
39     ; TELECOMMUNICATION INFORMATION:
40     ; TELEPHONE: (512) 418-3000
41     ; TELEFAX: (512) 474-7577
42     ; INFORMATION FOR SRD ID NO: 6:
43     ; SEQUENCE CHARACTERISTICS:
44     ; LENGTH: 926 base pairs
45     ; TYPE: nucleic acid
46     ; STRANDEDNESS: single
47     ; TOPOLOGY: linear
48     ;
49     ; FEATURE:
50     ; NAME/KEY: CDS
51     ; LOCATION: 135..836
52     ;
53     ; US-08-470-670A-6

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Query Match 22.5%; Score 131; DB 2; Length 926;  
Best Local Similarity 56.3%; Pred. No. 2.2e-25;  
Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

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   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
424 ttgacactgctgacgagcggcgacatttcaactgacatccacgtccacatcaccc 483
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
218 gctcagccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 277
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278 ggggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 337
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544 ggggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 603
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338 aggaagatgagacacacacacacacacacacacacacacacacacacacacac 397
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
604 aggaagatgagacacacacacacacacacacacacacacacacacacacacac 663
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
398 ggcgtgctgacgtgacgtgacgtgacgtgacgtgacgtgacgtgacgtgacgt 457
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664 acctagagccttgatgacgagacgagacgagacgagacgagacgagacgagac 723
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
458 acggagcctctgagagagagagagagagagagagagagagagagagagagag 517
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724 acatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 783
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784 gcattgactgtgccc 798

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RESULT 7  
US-08-481-739-1  
Sequence 1, Application US/08481739  
Patent No. 6143291

GENERAL INFORMATION:  
APPLICANT: June, Carl H. and Thompson, Craig B.  
TITLE OF INVENTION: METHODS FOR ENHANCING T CELL SURVIVAL  
TITLE OF INVENTION: BY AUGMENTING BCL-XL PROTEIN LEVELS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/481,739  
FILING DATE: 07-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/435,518  
FILING DATE: 04-MAY-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Deconli, Giulio A. (GMD)  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: RPI-034CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:

LENGTH: 926 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 135..836  
US-08-481-739-1

Query Match 22.5%; Score 131; DB 3; Length 926;  
Best Local Similarity 56.3%; Pred. No. 2.2e-25;  
Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

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98 ccggagagagccagcagcagcagcagcagcagcagcagcagcagcagcagcagc 157
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364 cccggagagtgatgccatgscagcaagcaagcgtgagagagcagcagcagcagcag 423
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158 tcgagaccgctccgagcagcctctctgacgtcgagcgtcagcgtcagcgtcagc 217
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424 ttgacactgctgacgagcggcgacatttcaactgacatccacgtccacatcaccc 483
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218 gctcagccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 277
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338 aggaagatgagacacacacacacacacacacacacacacacacacacacacac 397
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604 aggaagatgagacacacacacacacacacacacacacacacacacacacacac 663
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398 ggcgtgctgacgtgacgtgacgtgacgtgacgtgacgtgacgtgacgtgacgt 457
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664 acctagagccttgatgacgagacgagacgagacgagacgagacgagacgagac 723
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458 acggagcctctgagagagagagagagagagagagagagagagagagagagag 517
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724 acatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 783
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518 tgcgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 532
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784 gcattgactgtgccc 798

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RESULT 8  
US-09-167-921-1  
Sequence 1, Application US/09167921A  
Patent No. 6172216

GENERAL INFORMATION:  
APPLICANT: Bennett, C. Frank  
APPLICANT: Dean, Nicholas M.  
APPLICANT: Monia, Brett P.  
APPLICANT: Nickoloff, Brian J.  
APPLICANT: Zhang, Qingqing  
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression  
FILE REFERENCE: ISPH-0324  
CURRENT APPLICATION NUMBER: US/09/167,921A  
CURRENT FILING DATE: 1998-10-07  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1  
LENGTH: 926  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (135)..(836)  
PUBLICATION INFORMATION:  
DATABASE ACCESSION NUMBER: L20121 Genbank





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QY 518 tgctgacggggcg 532  
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Db 784 gcatgactgtgccc 798

RESULT 11  
US-08-461-511A-6  
Sequence 6, Application US/08461511A  
Patent No. 6303331  
GENERAL INFORMATION:  
APPLICANT: Thompson, Craig B.B.  
Boise, Lawrence H.  
TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS  
AND METHODS  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,511A  
FILING DATE: 05-Jun-1995  
CLASSIFICATION: UNKNOWN  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: ARCD:179  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 926 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 135..836  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-08-461-511A-6

Query Match 22.5%; Score 131; DB 4; Length 926;  
Best Local Similarity 56.3%; Pred. No. 2.2e-25;  
Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

QY 98 ccggagagcccgccagcagctgacccgctgcaaccaagacatgctggagctgagatgagt 157  
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Db 364 CCCGGAGGTGATGCCCTCCAGGAGCAGTAAAGCAAGCGCTGAGGAGCGACGCGAGAGT 423  
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Db 424 ttgaactgcggatccgggggagcttcaatgacatgacatccacatccatccatccatcc 483  
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QY 458 acggggcccttgagagcgcgcgctctcgtggaaggggaactggcatcagtggagacag 517  
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Db 724 ACAATGACGAGCGCGAGAGCGCGGAAAGGGCCAGGACGCTTCAACCGCTGCTCTGACG 783  
QY 518 tgctgacggggcg 532  
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Db 784 gcatgactgtgccc 798

RESULT 12  
PCT-US94-07089-6  
Sequence 6, Application PC/TUS9407089  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Vertebrate Apoptosis Gene:  
TITLE OF INVENTION: Compositions and Methods  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: TX  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS, ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/07089  
FILING DATE: CONCURRENTLY FILED  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/081,448  
FILING DATE: 22 JUNE 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: PARKER, David L.  
REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: ARCD090  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-789-2679  
TELEFAX: 713-789-2679  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 926 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 135..836  
PCT-US94-07089-6

Query Match 22.5% Score 131; DB 5; Length 926;  
Best Local Similarity 56.38; Pred. No. 2.2e-25;  
Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

QY 98 ccgggaggggcccagcagctgaccgctgcccacagccatgcccagggagagatgact 157  
DB 364 cccgggagctgattccctgacagcagcagcagcagcagcagcagcagcagcagc 423  
QY 158 tcgaaaccgctccgagcagcctctctgctgagcagcagcagcagcagcagcagc 217  
DB 424 ttgaactgctgacccgagcagcagcagcagcagcagcagcagcagcagcagcagc 483  
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QY 338 aggaagatgaaacacagctgagcagcagcagcagcagcagcagcagcagcagc 397  
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QY 518 tcctgagcggggggc 532  
DB 784 gcatacgtggtggc 798

RESULT 13  
US-08-465-485A-20  
Sequence 20, Application US/08465485A  
Patent No. 5831066  
GENERAL INFORMATION:  
APPLICANT: Reed, John  
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
ADDRESS: P.C.  
STREET: 1755 S. Jefferson Davis Hwy., Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,485A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 514  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/124,256  
FILING DATE: 20-SEP-1993  
PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 07/840,716  
FILING DATE: 21-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/288,692  
FILING DATE: 22-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Fortney, Andrew D.  
REGISTRATION NUMBER: 34,600  
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (408) 436-2070  
TELEFAX: (408) 436-2075  
INFORMATION FOR SEQ. ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 717 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..717  
US-08-465-485A-20

Query Match 21.2% Score 123.4; DB 2; Length 717;  
Best Local Similarity 58.68; Pred. No. 1.9e-23;  
Matches 214; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

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DB 604 tacgg 608

RESULT 14  
US-09-080-285-20  
Sequence 20, Application US/09080285  
Patent No. 6040181  
GENERAL INFORMATION:  
APPLICANT: Reed, John  
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
ADDRESS: P.C.  
STREET: 1755 S. Jefferson Davis Hwy., Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.



Thu Jun 6 16:39:18 2002

us-09-155-327e-6.rni

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Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute; 1-7-22 Suenhiro-cho, Tsunumi-ku, Yokohama  
Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)  
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for  
further details.

cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in Riken.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues. First strand cDNA was primed with a primer  
[5'] GAGAGGACGAGCGGCCGCACACTGGATTTTCTTTTTTNN 3'), cDNA was  
prepared by using Triclose thermo-activated reverse transcriptase  
and subsequently enriched for full-length by cap-trapper. Second  
strand cDNA was prepared with the primer adapter of sequence [5']  
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cleaved with XhoI and SacII. Cloning sites, 5' end: SstII; 3' end:  
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FEATURES  
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Location/Organisms  
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/strain="C57BL/6J"  
/db\_xref="MGI:MGI:1896837"  
/db\_xref="taxon:10090"  
/clone="1200009L24"  
/sex="male"  
/tissue\_type="lung"  
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/dev\_stage="adult"  
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209..790  
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data source:MGI, source key:MGI:108052, evidence:ISS  
putative"

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CDS  
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polyA\_site  
BASE COUNT 777 a 834 c 990 g 886 t  
ORIGIN

Query Match 90.5%; Score 527.6; DB 11; Length 3487;  
Best Local Similarity 94.2%; Pred. No. 1,4e-109;  
Matches 548; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

1 atggcgaaccccaagcttcgagcgccccaagaacaagggtcttgtagcagaacttttagtgtat 60  
|||||  
209 ATGGCGACCCACCACCTCAACCCCBAACAACAGGGGCTCTAGTGCTGACTTGTGAGGCTAT 268  
61 aagctgagcagaaggttatctctgttgtagagtgcgccggggaaggaccacaagctaac 120  
|||||  
269 AAGCTGAGCGAGAAGGTTATGTCGTGTGAGACTGCGCCCTGGGAAGCCACCACCGCAC 328  
121 ccgctgacacaaagcatctgcgggcagctctggagatgattcagagaccgccttcgcgcgac 180  
|||||  
329 CCGCTGACCAACCCATWGCGGGCTCTGGAACAAGATTGAGACCCGTTTCCGCCGCACAC 388  
QY ttctcgtatctgcgcctcagctgatctgtgccccagaagcccaagcagaagcttaac 240  
Db TTCTCMTACCTGGCGCTAGCTTACACTAGTACCCCAAGGCTACACCCAGCAAGCTTTCAC 448  
241 caggtctcgaagcaatttcaagaaggggcccacaactcgggaccttgtaagcttctt 300



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|||||
Db 449 CAGGTTTCGACGACACTTTCCAAAGGGGGCCCAACTGGGGCGCTCTGTGCAATCTTT 508
Oy 301 gtcttgaggctgcaactgtgtctgagagtgtaacaagaagatggaaccactgtgtga 360
Db 509 GTCTTTGGGGGTGCGCTGTGCTGAGAGTGTCAACAAAGAAATGAGGCTTTGGTGGGA 568
Oy 361 caagtgcagagatgagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 420
Db 569 CAAGTGCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 628
Oy 421 agtggagctgagcagatcaacagctctatacagggagcggcctgtgagagagcgag 480
Db 629 AGTGGGGCTGTGGGGAGTTCACAGCTCTATACGGGAGCGGGCCCTGGAGAGGACAGG 688
Oy 481 cgtctcgagggaggaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 540
Db 689 CGTCTGCGGAGGAGGAGTGGGCACTGAGTGAAGAGTGTGTGTGTGTGTGTGTGTGTGT 748
Oy 541 gggggcctgtaactgtagggcccttttctgttagcaagtaga 582
Db 749 GGGGCCCTGCTACTGTAGGGGCTTTTTCCTAGCAAGTGA 790

RESULT 5
Bi770566 697 bp mRNA linear EST 25-SEP-2001
LOCUS 603060362F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5209862 5'
DEFINITION mRNA sequence.
ACCESSION Bi770566
VERSION Bi770566.1 GI:15762144
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 697)
AUTHORS NIH-MGC http://mhc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM1526 row: k column: 15
High quality sequence start: 21
Location/Qualifiers
1. 697
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5209862"
/clone_id="NIH_MGC_122"
/lab_host="DH108"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invited). Research Genetics tracking code 026. Note:
this is a NIH-MGC Library."
BASE COUNT 121 a 202 c 248 g 126 t
ORIGIN

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Query Match 83.7%; Score 488.2; DB 10; Length 697;
Best Local Similarity 98.6%; Pred. No. 7.9e-101;
Matches 345; Conservative 0; Mismatches 3; Indels 5; Gaps 5;

Oy 1 atgagcaccacccagccttcgcccagacacacagcgtctgtgtgagactgttaggtat 60
Db 145 ATGCGACCCAGCAGCTTCGCGCCAGACACAGGGGCTGTGTGTGTGTGTGTGTGTGT 204
Oy 61 aagctgagcagaaaggatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 120
Db 205 AAGCTGAGGCGAAGAGGTTTATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 264
Oy 121 ccgctgcacacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
Db 265 CCGCTGCACCAAGCCATGCGGGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 324
Oy 181 ttctctgattcggaggtcagctcagctcagctcagctcagctcagctcagctcagctc 240
Db 325 TTTCTGTATCTGGGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 384
Oy 241 caggtctccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300
Db 385 CAGGCTCCGAGTGAACCTTTTCAAGGGGGGCCCAACTGGGGCCCTTTGTAGCTTTT 444
Oy 301 gtcttgaggctgcaactgtgtctgagagtgtaacaagaagatggaaccactgtgtga 359
Db 445 GTCTTTGGGGGTGCGCTGTGCTGAGAGTGTCAACAAAGAGATGGAACACACTGTGTG 504
Oy 360 acaagtgcagagatgagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 418
Db 505 ACAGTGCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 564
Oy 419 gcaagtggagctgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 477
Db 565 GCAGTGGGGCTGCGCGGAGTTCACAGCTCTATACGGGAGGAGGAGGAGGAGGAGG 624
Oy 478 cggcgtctcgagagagcagcagcagcagcagcagcagcagcagcagcagcagcagc 535
Db 625 CGGCGTGTGGGAGGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 684
Oy 536 cactgaggagcct 548
Db 685 CACTGGGGGCGCT 697

RESULT 6
Bi910270 643 bp mRNA linear EST 16-OCT-2001
LOCUS 603069493F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5218294 5'
DEFINITION mRNA sequence.
ACCESSION Bi910270
VERSION Bi910270.1 GI:16173653
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 643)
AUTHORS NIH-MGC http://mhc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM1548 row: j column: 23
High quality sequence stop: 643.
Location/Qualifiers

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1. 643
/organism="Homo sapiens"
/db.xref="taxon:9606"
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/lab_host="DH10B"
/notes="Vector: pCMV-SPORT6; Site.1: NotI; Site.2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."

BASE COUNT      129 a      184 c      216 g      114 t
ORIGIN

```

```

Query Match      72.5%  Score 422.4; DB 10; Length 643;
Best Local Similarity 94.3%; Pred. No. 6.7e-86;
Matches 449; Conservative 0; Mismatches 26; Indels 1; Gaps 1;

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QY 1 atggcgaacccagcctgagccagacacagcctgctgctgacacttgaattat 60
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Db 140 ATGGCGACCCAGCCTGCGCCCGACACAGCGGCTCTGTGGCAGACTTTGAGCTTAT 199
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QY 61 aagctgagcagaaggatgtctgtgagctgagcccgaggagagccagcagctgac 120
    |||||||
Db 200 AAGCTGAGCGAGAGGGGTATGTGTGAGAGTGGCCCGGGAGAGGCCACAGCTGAC 259
    |||||||

QY 121 ccgctgacacaaacacatgagcagctgagatgagatcagagccgcttcgagcagac 180
    |||||||
Db 260 CCGCTGACCAAGCAAGCGGCAAGTGAAGATGATGAGAACCCGCTTCGGCGACAC 319
    |||||||

QY 181 ttctctatctgagcagctcagcagcagctgagccagctcagcagcagcagcagc 240
    |||||||
Db 320 TTCTCTGATCTGCGCGCTGAGTGTGATGACCCAGCTCAGCCCAACAGCGCTTACC 379
    |||||||

QY 241 caggtccgagcgaacttttcaaggaggcccaactgagcagcttgaagctctt 300
    |||||||
Db 380 CAGGCTCGATGACTTTTTCAGAGGGGCCCCCACTGGGCGCGCTTGTAGCCTTCTTT 439
    |||||||

QY 301 gctcttgagcctgactgtgtgtgaggtgtcacaaggag-atggaacacatggtgag 359
    |||||||
Db 440 GTCTTTGGGCTGCACTGTGTCTGAGACTGTCAACAAGAGCATGGAACCATGTGGGG 499
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QY 360 acaagtcagcagatgagtgatgagcctacacagcagcagcagcagcagcagcag 419
    |||||||
Db 500 ACAAGTCAGAGATGATGTGCTTACCTGAGACAGCGCGCTGTGACTGTGATCCACAG 559
    |||||||

QY 420 cagtgaggcctgagcagcagcagcagcagcagcagcagcagcagcagcagcag 475
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Db 560 CAGTGGGGCTGCGAGCTGGAAGCTATCAAGCTGAGTCAAGGATGAGAGAG 615
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RESULT 7
LOCUS      BF785386                815 bp      mRNA      linear      EST 12-JAN-2001
DEFINITION 60211172BP1 NCI CGAP_Kid14 Mus musculus cDNA clone IMAGE:4239798
ACCESSION  BF785386
VERSION     BF785386
KEYWORDS   5', mRNA sequence.
SOURCE     BF785386.1 GI:12090422
ORGANISM   house mouse.
            Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 815)
            NIH-MGC http://mgi.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)

```

```

COMMENT
Contact: Robert Strausberg, Ph.D.
Email: c9apb@fml.nhl.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM953 row: h column: 07
High quality sequence start: 3.
High quality sequence stop: 650.
Location/Qualifiers
1. 815
/organism="Mus musculus"
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Site.2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

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BASE COUNT      166 a      212 c      296 g      141 t
ORIGIN
Query Match      68.6%  Score 400.2; DB 10; Length 815;
Best Local Similarity 91.4%; Pred. No. 7.8e-81;
Matches 502; Conservative 0; Mismatches 36; Indels 9; Gaps 7;

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QY 81 tgcctgagcagcgtgcccggaggagccagcagcagcagcagcagcagcagcagcag 140
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Db 61 TGCTGTGAGAGCTGGCCCTGGGGAAGGCCACCCGACCCGCTGACACCAAGCATGGC 120
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QY 141 ggcagctgagatgagcttgcagacccgcttcgagcagcagcagcagcagcagcag 200
    |||||||
Db 121 GCGTCTGAGAGACAGATT-CAGACCCGTTTCGCGCGACCTTCTGTACCTGGCGCTCA 179
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QY 201 gctgcatgacccccagcgttcagccagcagcagcagcagcagcagcagcagcagc 260
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Db 180 GCTACACGTGACCCAGAGCTCAGCCACAGACCGCTTACCCAGGTTTCCGACGAATTTT 239
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QY 261 tcaaggaggcccaactgaggccgagcagcagcagcagcagcagcagcagcagcag 320
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Db 240 CCAAGGGGCGCCCTTAACTGGGCGCTTGTGGCAFTTC---TGCTTGGGGCTGCTG 296
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QY 381 ggcctaccttgagagcagcagcagcagcagcagcagcagcagcagcagcagcagc 440
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Db 356 GGCTTACCTGAGAGACAGCTGTGCTGACTGTGATTCACAGAGTGGGGCTGGGAGATT 415
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QY 441 cagagcctatacagggagcagcagcagcagcagcagcagcagcagcagcagcagc 500
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Db 416 CACAGCTTATACGGGAGCGGGGCGCTGAGAGGACAGG-GTCTCGGGAGGGAGAC-G 473
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Db 474 GGCTACAGTGAAGACATGCTGTGAGCGGGGCGGTGGAGCT-GGGGCGCTGTAACTGATG 532
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QY 561 ggcctttt 569
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Db 533 GGCTTTT 541
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RESULT 8  
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LOCUS AK013244  
DEFINITION Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length  
enriched library, clone:2810435A13:Bcl2-like 2, full insert  
sequence.  
ACCESSION AK013244  
VERSION AK013244.1 GI:12850487  
KEYWORDS HNC: CAP trapper.  
SOURCE Mus musculus (strain:C57BL/6J) 10, 11 days embryo cDNA to mRNA,  
clone:lib-RIKEN full-length enriched mouse cDNA library  
clone:2810435A13.  
ORGANISM Mus musculus  
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Eukaryota; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (sites)  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636  
REFERENCE 2 (sites)  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
TITLE JOURNAL  
MEDLINE 20499374  
PUBMED 11042159  
AUTHORS 3 (sites)  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Kono, H., Akiyama, J., Nishi, K., Katsunuma, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuyama, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multichannel sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
TITLE JOURNAL  
MEDLINE 20530913  
PUBMED 11076661  
AUTHORS 4 (sites)  
The RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)  
5 (bases 1 to 854)  
Adechi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A.,  
Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C.,  
Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T.,  
Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hirakawa, T., Hori, F.,  
Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Katsunuma, T.,  
Kato, H., Kawai, J., Kojima, Y., Kono, H., Kouda, M., Koya, S.,  
Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K.,  
Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J.,  
Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,  
Schriml, L., Shibata, K., Shibata, Y., Shingawa, A., Shiraki, T.,  
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,  
Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamakawa, I.,  
Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and  
Hayashizaki, Y.  
Direct Submission  
Submitted (10-JUN-2000) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suenho-cho, Tsukuba, Ibaraki,  
Kanagawa 230-0045, Japan (E-mail:genome-res@gs.c.riken.go.jp,  
URL: http://genome-gsc.riken.go.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)  
Please visit our web site (http://genome-gsc.riken.go.jp/) for  
further details.  
cDNA library was prepared and sequenced in Mouse Genome

## FEATURES

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196..732  
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BASE COUNT 178 a 229 c 264 g 183 t  
ORIGIN

Query Match 65.28; Score 380.2; DB 11; Length 854;  
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316 CCGCTGACACCAAGCCATGTGGGCTCTGTGAGAGACCGCTTCCCGGACG 375  
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376 TTCTTGACCTGCGCTGAGCTACAGCGACCGACGCTGAGCCAGCAGCTTACG 435  
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436 CAGGTTCCGACGACACTTTTCCAGAGGGGCCCTAAGTGGCGCGCTGTGCAATCTTT 495  
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361 caagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 420  
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556 CAAGTGAGGAGTTTGATGATGAGGCTGCTGAGACACAGCTGCTGACTGATCAGAC 615  
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421 agtgaggcctgagg 433



Matches 394; Conservative 0; Mismatches 35; Indels 1; Gaps 1;

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 QY 121 ccgctgacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180  
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 QY 301 gtcttgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 360  
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 Db 412 GTCTATGGGCTGCTGCTGTGCTGAGAGTGTACAAAGAAATGAGCCTTTGGTGGGA 471  
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 QY 361 caagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 420  
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 Db 472 CAACTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 530  
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 QY 421 agtgggggct 430  
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 Db 531 AGTGGGGCT 540  
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RESULT 11  
 B1764428 758 bp mRNA linear EST 25-SEP-2001  
 LOCUS 603050701F1 NIH\_MGC\_116 Homo sapiens cDNA clone IMAGE:5190792 5',  
 DEFINITION mRNA sequence.  
 ACCESSION B1764428  
 VERSION B1764428.1 GI:15756006  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 758)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: cgaapb-remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LLM11477 row: a column: 01  
 High quality sequence stop: 753.  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:5190792"  
 /clone\_1ib="NIH\_MGC\_116"  
 /lab\_host="DH10B"  
 /note="Organ: pooled colon, kidney, stomach. Vector:  
 pcMV-SPORE6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA  
 source anonymous pool of 3 colons, age 26 yo male, 49 yo  
 female, 71 yo male colon; 46 yo male kidney, and pool of 2

stomachs, 62 yo male and 70 yo female. library is  
 oligo-dT primed and directionally cloned (EcoRV site is  
 destroyed upon cloning). Average insert size 1.4 kb,  
 insert size range 1-3 kb. library is normalized and  
 enriched for full-length clones and was constructed by C.  
 Gruber (Invitrogen). Research Genetics tracking code  
 023. Note: this is a NIH-MGC Library."

BASE COUNT 140 a 216 c 228 g 174 t

ORIGIN

Query Match 56.3%; Score 328.4; DB 10; Length 758;  
 Best Local Similarity 98.2%; Pred. No. 1.3e-64;  
 Matches 332; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 atgggagacccagcctcgcccccagacacacagcgtctgtgtgacagactttagttat 60  
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 Db 139 ATGGGAGACCCAGCCTCAACCCAGACACAGGGGCTCTAGTGGCTGTGTTGAGCTAT 198  
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 QY 61 aagctgaagcagaaggtatgtctgtgagcttgccccgggagggccagcagctgac 120  
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 Db 199 AAGCTGAGGCAAGAGGTTATGTCTGTGAGCTTGCCCTGGGGAGAGCCAGCAGCTGAC 258  
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 QY 121 ccgctgacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180  
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 Db 259 CCCTGACACCAAGCAGTGGGGCTCTGAGACAGAGTTTGAACCCGTTCCGCCGAC 318  
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 QY 181 tctctgacatcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 240  
 |||||  
 Db 319 TTCTGTGATGAGCAGTGGGGCTCTGAGAGTGTACAAAGAAATGAGCCTTTGGTGGGA 378  
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 QY 241 caagctccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300  
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 Db 379 CAGGTTCCGACCACTTTTCCAGGGGGGCTTAACTGGGGCGCTGTGGCAATCTTT 438  
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 QY 301 gtcttgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 338  
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 Db 439 GTCTTGGGCTGCTGCTGTGCTGAGAGTGTTCAG 476  
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RESULT 12  
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 DEFINITION mRNA sequence.  
 ACCESSION BF204905  
 VERSION BF204905.1 GI:11098491  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 601)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: cgaapb-remail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov  
 Plate: LLM987 row: d column: 05  
 High quality sequence stop: 561.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4106836"  
 /clone\_1ib="NIH\_MGC\_17"  
 /tissue\_type="rhodomyosarcoma"







Thu Jun 6 16:39:19 2002

us-09-155-327e-6.rst

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FEATURES	Hospital, Parkville, Victoria 3050, Australia
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	1. .582
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	/db_xref="taxon:3606"
	/chromosome="14"
	/map="14q11"
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	/gene="bcl-w"
CDS	1. .582
	/gene="bcl-w"
	/note="promotes cell survival"
	/codon_start=1
	/product="Bcl-w"
	/protein_id="AAB09055.1"
	/db_xref="GI:1572493"
	/translation="MATPASAPDTRALVADPEVGYKLRKGYVCGAGEGEPAPADPLHQ
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	RLRGCAVSNVRYVITGTGVALGVALTGTGAFFPAK"
BASE COUNT	104 a 156 c 211 g 111 t
ORIGIN	

Query Match	99.8%	Score 582	DB 9	Length 582
Best Local Similarity	100.0%	Pred. NO. 4.1e-119		
Matches 582	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	atggcaccacccagcctctcggccccagacacacgagcctctgtgtgcagacttgaagttat	60	
Db	1	ATGGCACCCACACCTTCGGCCCCAGACACACAGGGCGCTCTGTGGACACTTTGTAGTTAT	60	
QY	61	aagctgaaggcagagaaggtatgtctgtgaagctcggccccggggaagggccccagactgac	120	
Db	61	AAGCTGAGGCAGAGAGGCTTATGCTGTGTGGAGCTGGCCCCGGGAGGGCCCCACACTGAC	120	
QY	121	ccgctgcaccaaagccatctgcggcagcttgagatgaattcgaagaccgcttcgcggcacc	180	
Db	121	CCGCTGCACCAAGCCATGCGGGCAGCTGAGATGATGATTGAAACCCGCTTCGGGGCACC	180	
QY	181	tctctgactctgcggcctcgaactgataatgtgacccccagctcagccccagacgcttcacc	240	
Db	181	TTCTCTGANTCTGGCGGCTTAGCTAGCTGTGACCCACAGGCTCAAGCCAGCAACGCTTCACC	240	
QY	241	cagatctccgaagaaacttttcaagggggccccaaactggcgccgacttgtagccttcctt	300	
Db	241	CAGGCTCTCGAGCAACTTTTCAAGGGGGCCCCAACTGGGGCGGCTTGTAGCCTTCTTT	300	
QY	301	gaccttggggcgccgacctgtgtctgaaggtgtgtcaacaaggagatgnaaacacttgatgga	360	
Db	301	GCTCTTTGGGGCGCTGCACTGTGTCTAGAGTGTCAACAAGGAGATGAAACCACTGGTGGA	360	
QY	361	caaatgcaggagatggaatgtgtgacctaaccttgaagacgcgcctgcgacttgatccacagc	420	
Db	361	CAAGTGCAGAGAGATGATGTGGCTTACCTGGAGAGCGGCGTGCATGTGATTCACACAGC	420	
QY	421	agtgaggacctggcggaattcaacagctctatacgggagacggggccctgaggaagcgcg	480	
Db	421	AGTGAGGAGCTGGCGGAGATTCAACACTTTATACGGGGAGCGGGCCCTGAGAGAGCGCGG	480	
QY	481	cgctctcgggaggggaaacttgatcgaatgagagacagatgctgcgacgagggccgttgaccatg	540	
Db	481	CGTCTCGGGAGGGGAACTGGGCATCAATGAGAGACAGTCTGACAGGGGGCCGTGACACTG	540	
QY	541	ggggccctcggtaaactgtatggggcctttttgtctagcaagta	582	
Db	541	GGGGCCCTCGTAACTGTAGGGGCCCTTTTGTCTAGCAAGTA	582	

ACCESSION D87461  
 VERSION D87461.1 GI:1944417  
 KEYWORDS KIA0271.  
 SOURCE Homo sapiens male brain myeloblast cell line:KG-1 CDNA to mRNA, clone\_1lib:psPort 1 clone:HA6752.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 3542)  
 Nagase,T., Seki,N., Ishikawa,K., Ohira,N., Kawarabayasi,Y., Ohara,O., Tanaka,A., Kotani,H., Miyajima,N. and Nomura,N.  
 Prediction of the coding sequences of unidentified human genes. VI. The coding sequences of 80 new genes (K1A0201-K1A0280) deduced by analysis of cDNA clones from cell line KG-1 and brain  
 JOURNAL DNA Res. 3 (5), 321-329 (1996)  
 MEDLINE 97191544  
 REFERENCE 2 (bases 1 to 3542)  
 Ohara,O., Nagase,T., Kikuno,R. and Nomura,N.  
 Direct Submission  
 JOURNAL Submitted (27-AUG-1996) Osamu Ohara, Kazuo DNA Research Institute: 1532-3, Yana, Katsuzaki, Chiba 297-0012, Japan  
 (E-mail:cdnainfo@kazuo.or.jp, Tel:+81-438-52-3913)

FEATURES	Location/Qualifiers
source	1..3542
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="HA6752"
	/sex="male"
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	/cell_type="myoblast"
	/tissue_type="brain"
	/clone_lib="psf01"
	177..758
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CDS	/gene="KIAA0271"
	/note="similar to human transforming protein bcl-2 (A24428)"
	/codon_start=1
	/protein_id="BA19666.1"
	/db_xref="gi:1944418"
	/translation="MAPKAPADPRALVADPVGKYLROKGYVCGAGPESPAADPLHQA AMRAAGDEFFRRFRFTSDLAALOHVTPGSAOORPTQVSDLPFGGPMKGLVAFVR GAALCAESVNEEMELVNGOVQVNVAYLEPLIAMIHSSGMAEPTALYIGDALAEAR RLRNSNMSVTVTVTGVALGALVTVGAFFSK"
BASE COUNT	804 a 817 c 1030 g 891 t
ORIGIN	
Query Match	99.5%; Score 579.8; DB 9; Length 3542;
Best Local Similarity	99.7%; Pred. No. 1..le-118;
Matches 581; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 atggtcgaaccgaagctcggtgccccagacacacagcgcgtctgtgtgcagacttttagtattat 60
Db	177 AAGGCGACCCCAAGCTCGCGCCCCCAACACACAGCGGCTGTGTGCAGACTTGTAGCTTAT 236
QY	61 aagctgagcgagaaggtatgtctgtgtgaagctggccccggggggggggcccgacgctgac 120
Db	237 AAGCTGAGCGAGCAAGAGGTTATGTCTGTGAGAGTGGCCCCGGGGAGGGCCACAGCAAGCTTAC 296
QY	121 ccgctgcaccaaagccatgcygggcagctgtgagatgagtgcgaagccgcttcgcgcgacac 180
Db	297 CCGCTGCACCAAGCCCATCGGGGCGAGCTGAGATGATGTTCCGAGACCCGCTTCGGGGCAGCC 356
QY	181 ttctctgattcggggcctcaagctgcattgtgaccccaagcttaagcccgacaaagcttaacc 240
Db	357 TTCTCTGATCTGGGGGCTCAAGCTGATGTGACCCCAAGGCTCAAGCCCAACAGCTTCAAC 416
QY	241 caagctcccgacgaacttttcaaggggggcccccaacgcyggggcgcgctttagccttcctt 300
Db	417 CAGGTCGCCATGAACCTTTTCAAGGGGGGCCCAACTGAGGGGGCCCGCTTGTGACCTTCTTT 476

	301	360	360
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Db	gtcttttggggctgcacctgtgtctgaagatctcaacaaaggaaatggaaacacacttggttggaa	536	
OY	caagtgcagagatgtgatgtgtgtcctacctagagacgcggtctgtcttgatctgattccacagc	420	
Db	caatgcacagagatgtgatgtgtgtcctacctagagacgcggtctgtcttgatctgattccacagc	596	
OY	agtgagggctgtgggcggagattcacagctctatcacggagacgggcctctgaagagagcgcg	480	
Db	agtgagggctgtgggcggagattcacagctctatcacggagacgggcctctgaagagagcgcg	596	
OY	agtgagggctgtgggcggagattcacagctctatcacggagacgggcctctgaagagagcgcg	480	
Db	agtgagggctgtgggcggagattcacagctctatcacggagacgggcctctgaagagagcgcg	596	
OY	ctctctcggagaggaactctgtgcattcaatgtgaagacaatgtctgacggggccgtggcacttg	540	
Db	ctctctcggagaggaactctgtgcattcaatgtgaagacaatgtctgacggggccgtggcacttg	716	
OY	ggggccctgtgaactgtatgagggccttttttctagcaagttaa	583	
Db	ggggccctgtgaactgtatgagggccttttttctagcaagttaa	759	

RESULT	3			
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LOCUS	AX022529	583 bp	DNA	linear
DEFINITION	Sequence 6 from Patent EP0932674.			
ACCESSION	AX022529			
VERSION	AX022529.1	GI:10046125		
KEYWORDS	.			
SOURCE	unidentified.			
ORGANISM	unclassified.			
REFERENCE	1 (bases 1 to 583)			
AUTHORS	Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.			
TITLE	A novel mammalian gene, bcl-w, belongs to the bcl-2 family of apoptosis-controlling genes			
JOURNAL	Patent: EP 0932674-A 6 04-AUG-1999;			

FEATURES	Location/Qualifiers
source	1..583 /organism="unidentified" /db_xref="taxon:32644"
CDS	1..583 /note="unnamed protein product" /codon_start=1 /protein_id="CAC07880.1" /db_xref="GI:10046126" /translation="MATPASPDPTRALVADFVGYYKIRQKGYCGAGPGEHPAADPLH NARAGDEFETFRFRFTSDIAQLVHTPPSSAQORTQVSDLFPGGPMNGRLVATFLL GALCAESYNKEMEPYGVQOEMWVALEYTRLDVTHSSGGMAEFTALYGDALDEEA RLREGMVASRVTLVGCVALGALVTVGAFASF"
BASE COUNT	105 a 157 c 210 g 111 t
ORIGIN	

Query Match	99.2%	Score 578.2	DB 6	Length 583
Best Local Similarity	99.5%	Pred. No. 2.8e-118		
Matches 580; Conservative	0	Mismatches 3	Indels 0	Gaps 0

Qy	1	atggcgcagcccaagctctgcgcccccaagaaacacagggctcttggttggagaagactcttgatggctac	80
Db	1	ATGGCGACCCACAGCTTGCGGCCCCAGAACACAGGGCTCTGGTGGCAGACTTGTAGGTTAT	60
Qy	61	aagctgagagcaagaagggtatattgtctgtgagactgtgccccggggagagcccaagcagctgcac	120
Db	61	AAGCTGAGGCAAGAGGGATTATGCTGTGGAGACTGGCCCCGGGGAGAGGGCCAGCGAGCTGAC	120
Qy	121	cgcgtgcacccaagccatgtgcggcgacgctggaagatgagtttcgagaccgcgtcttcggcgagacc	180
Db	121	COGCTGCACCAAGCCATGCGGGCAGCTCGAATGAGTTCGAGACC CGCTTCGGCGGCACC	180
Qy	181	ttctctgatcttggcgagctcaagctgcatgtgagcccccaagctcaagcccaagcaagcgttaacc	240
Db	181	TTCTCTGATCTGGCGGCTCAAGCTGATGTGAGCCCCAAGGCTCAAGCCACCAACGCTTCAAC	240

QY	241	caagtcgccacagacacttlttcaaggggcccacaactgaggcgccctttagcccttltt	300
Db	241	CAGGTCGCCGACGAACCTTTTCAAGGGGGCCCCAACGCGGGCCCCCTTGAGCCCTTCTTT	300
QY	301	gtctttgggagctgcactgltgttcgtgaagtgctacaagaagatagagaccactgtgtgga	360
Db	301	CTCTTTGGGGCGCTGCACCTGTGCTGGAAGTCTCAACAAAGGAGATGGAACCACTGCTGGGA	360
QY	361	caagtgcagagatgtagatgtgtgctactactgtagacagcgcgctgtgctgtactgataccagc	420
Db	361	CAAGTCAGAGAGTGAGTAGTGCGCTACTCTGGAAGACCGGGCTGTCGACTGGATCCACAGC	420
QY	421	agtgaggagctggcgagagttcacagctctatacggggagcgggccctggaggaagcgcg	480
Db	421	AGTGGGGCGCTGGCGGAGTTCAACAGCTTAAACGGGGAGCGGGCCCTGGAGAGGCGGG	480
QY	481	cgtctgcggagggagaaactgtagcctcagtaggaagaagtgctgcacggagggcgctgtgcactg	540
Db	481	CGTTCGCGGGAGGGGAACCTGGGCATCTGAAGAGACAGTCTGACCGGGCGCTGGCACTG	540
QY	541	ggggccctgatacctgtagggcccttlttctgtagcaagtga	583
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RESULT	4				
AX030817	AX030817	583 bp	DNA	linear	PAT 20-SEP-2000
LOCUS					
DEFINITION	Sequence 6 from Patent WO9335971.				
ACCESSION	AX030817				
VERSION	AX030817.1	GI:10278311			
KEYWORDS	.				
SOURCE	unidentified.				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 583)				
AUTHORS	Adams,D.M., Holmgren,S.P., Cory,S. and Gibson,L.M.				
TITLE	A novel mammalian gene, bcl-w, belongs to the bcl-2 family of apoptosis-controlling genes				
JOURNAL	Patent: WO 9735971-A 6 02-OCT-1997;				

FEATURES	source	location/Qualifiers
CDS	LEONIE M (AU) ; ANRAD OPERATIONS PTY LTD (AU)	1..583 /organism="unidentified" /db_xref="taxon:32644" 1..583 /note="unnamed protein product" /codon_start=1 /protein_id="CAC09621.1" /db_xref="GI:10278312" /translation="MATPASAPDTRALVAFVYKLRKGYCGAGPGEGSPADELH AARAAQDEFETRRPRTFSLAQLHVTTPSSAQRRTQVSDLEFPGGPNMGRVAFELL GALCAESVYKMEPELVQGVQEMVAVYETRLVDWTHSSGVAEFPALIXGDALBEA RLREGNMAVSRTVLGCAVALGALVTFGAFFASK"
BASE COUNT	105 a 157 c 210 g 111 t	
ORIGIN		

	Query Match	99.2%	Score 578.2;	DB 6;	Length 583;	
	best Local Similarity	99.5%;	Pred. No. 2,8e-118;			
	Matches 580; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0	
QY	1 atggcgcagcccccagctctcgccccagacacacagcgtcttgltgcaagaatttgttagttat					60
Db	1 ATGGCGCAGCCCCCAGCTCTGCCCCCGACACACAGSGSCTTGTGGCAGACTTTGTATGATTAT					60
QY	61 aaagtgcaggcgaagaaggttatgtcttcgtgcagcttggccccggggagggccaccagacttac					120
Db	61 AAGCTGAAGCGAAGAGGGTTATGTCCTGTGCAGACTGGCCCCGGGGAGGGGCCACAGCTAGTGAC					120
QY	121 ccgctgcaccacaagcatcgcggcagcttgcagatgatgatcgcagaccgcgcttcgcggcacc					180

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121 |CCCCCTCACCACCAAGCCATGGCGGAGCTGAGATGATCTGAGACCCGCTTCCGGCGCAC
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181 |ttctcgtatcgtgagcgtacgtcgtgtgacccagcgtcagccagcagcttacc 240
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481 |cgtctcggaggaggagcagcagcagcagcagcagcagcagcagcagcagcagc 540
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541 |ggggccttgtagttagttagttagttagttagttagttagttagttagttagt 583
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RESULT 5  
LOCUS BC021198 1437 bp mRNA linear PRI 22-JAN-2002  
DEFINITION Homo sapiens, BCL2-like 2, clone MGC:10675 IMAGE:3944307, mRNA, complete cds.  
ACCESSION BC021198  
VERSION BC021198.1 GI:18203706  
KEYWORDS MGC.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1437)  
Strausberg, R.  
Direct Submission  
Submitted (14-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: http://mgc.nci.nih.gov  
Contact: MGC help desk  
Email: cgaops-r@mail.nih.gov  
Tissue Procurement: DCTD/DRP  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: http://www.nisc.nih.gov/  
Contact: nisc\_mgc@nih.gov  
Shenoychenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M., Benjamini, B., Blakesley, R.M., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-D., Karlins, E., Legaspi, R., Lim, M., Maduro, Q.L., Mastello, C., Mastrian, S.D., McCloskey, V.C., McDowell, J., Pearson, R., Snyder, B., Stantrilpop, S., Thomas, P.J., Tjongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Zhang, L.-R. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov  
Series: IRML Plate: 15 Row: K Column: 19

FEATURES  
source  
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1. 1437  
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BASE COUNT 303 a 343 c 509 g 282 t  
ORIGIN

Query Match 99.2% Score 578.2; DB 9; Length 1437;  
Best Local Similarity 99.5%; Pred. No. 2,6e-118;  
Matches 580; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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1 atgcaaccccaagcctcgcagcagcagcagcagcagcagcagcagcagcagcagc 60
176 ATGCGACGCCACAGCCTCGGCCAGACACAGCGGCTCTGTGAGACTTTTGTAGTTAT 235
61 aagctgaagcagaaggtatgtctgtgagcgtgagcagcagcagcagcagcagc 120
236 AAGCTGAGGAGAGAGGATTATGCTGTGAGCTGGGCCCGGAGAGGCCACAGCTGAC 295
121 ccgctgacccaagcctcgcagcagcagcagcagcagcagcagcagcagcagcagc 180
296 CCAGTGCACCAAGCCATGGCGGAGCTGAGATGAGTTCGATCGAACCCGCTTCGGGCAAC 355
181 ttctcgtatcgtgagcgtcagcagcagcagcagcagcagcagcagcagcagcagc 240
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476 GTCTTGGGGGCTGCACTGTGCTGAGAGTGCACCAAGAGATGAGAACCACTGTGGA 535
361 caagtcgaagatgtagtggcctacccagcagcagcagcagcagcagcagcagc 420
536 CAAGTCGAGAGATGATGATGCTGCTGAGAGAGCGGCTGCTGATGATGATGATG 595
421 agtcgggagcgtgagcagcagcagcagcagcagcagcagcagcagcagcagc 480
596 ACTGGGGGCTGGCGGAGTTCACACTCTATACGGGAGCGGCGCTTGAGAGAGCGCG 655
481 cgtctcggaggaggagcagcagcagcagcagcagcagcagcagcagcagcagc 540
656 CGTCTGCGGAGAGGAGATGGCTGCTGCTGAGAGAGCGGCTGCTGATGATGATG 715
541 ggggcccctgtagttagttagttagttagttagttagttagttagttagttagt 583
716 GGGGCCCTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGT 758

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RESULT 6  
LOCUS AR020780 579 bp DNA linear PAR 05-DEC-1998









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 BASE COUNT 105 a 164 c 195 g 117 t  
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Query Match 86.8%; Score 505.8; DB 6; Length 581;  
 Best Local Similarity 91.9%; Pred. No. 3.2e-102;  
 Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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 OY 361 caagtgcagagatgtagttagtgcctacactgagagacgagcgtgtagttagtcaaac 420  
 DB 361 CAAGTCCAGAGATTGATGTGAGCTTACCTGAGACAGCTCTGCTGTGATCTGATCCAGC 420  
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 DB 421 AGTGGCGGCTGGGCGGAGCTTCAAGCTCTATACGGGAGCGGGCGCTGGAGAGCGACG 480  
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 DB 481 CGTCTGGCGGAGGAGCACTGGGCACTGAGTGAAGCAAGATGCTGAGGGGGCGCGTGACATG 540  
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 LOCUS DEFINITION Sequence 8 from Patent WO9735971.  
 AX030819  
 ACCESSION AX030819.1 GI:10278313  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 unclassified.  
 unclassified.  
 unclassified.

REFERENCE 1 (bases 1 to 581)  
 AUTHORS Adams,J.M., Holmgren,S.P., Cory,S. and Gibson,L.M.  
 TITLE A novel mammalian gene, bcl-w, belongs to the bcl-2 family of

## JOURNAL

apoptosis-controlling genes  
 Patent: WO 9735971-A 8 02-OCT-1997;  
 ADAMS JERRY MCKEE (AU) ; HOLMGREN SHAUN P (AU) ; CORY SUZANNE (AU)  
 ; GIBSON LEONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)  
 location/qualifiers

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 BASE COUNT 105 a 164 c 195 g 117 t  
 ORIGIN

Query Match 86.8%; Score 505.8; DB 6; Length 581;  
 Best Local Similarity 91.9%; Pred. No. 3.2e-102;  
 Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

OY 1 atggcgaccccaagcctcgcgcccagacacacagcgctcgtgtagcagacttgtagtat 60  
 DB 1 ATGCCGACCCCAAGCCTCAACCCAGACACACGCGCTCTAGTGCTGACTTTGTAGGCTAT 60  
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 DB 541 GGGGCGCTGTACTGTAGGGGCGCTTTTGTGTAGCAAGTG 581

RESULT 13  
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 LOCUS DEFINITION Human chromosome 14 DNA sequence BAC R-124D2 of library RFL-11  
 from chromosome 14 of Homo sapiens (Human), complete sequence.  
 ACCESSION AL049829  
 VERSION AL049829.4 GI:8217859



KEYWORDS HTG.  
SOURCE human.  
ORGANISM Homo sapiens  
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Eukaryota; Mollusca; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 196292)  
AUTHORS Heilig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Winkler, P.,  
Bottler, P., Catolico, L., Barbe, V., Pelletier, E., Artiguenave, F.,  
Levy, M., Eckenberg, R., Bruls, T., Debernardi, V., Cruaud, C.,  
Gyapay, G., Saurin, W., and Weissbach, J.  
TITLE Sequencing of the human chromosome 14  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 196292)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Genoscope - Centre National de Sequencage :  
Submitted (21-MAY-2001) Genoscope - Centre National de Sequencage :  
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
COMMENT On Jun 3, 2000 this sequence version replaced gi:6138746.  
----- Genome Center  
Center: Genoscope / Centre National de Sequencage  
Center code: GS  
Web site: http://www.genoscope.cns.fr/  
Contact: seqref@genoscope.cns.fr  
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The following BAC sequence is oriented from the T7 to the SP6 end.  
Upstream BAC (overlapping the T7 end) : R-244E17  
Downstream BAC (overlapping the SP6 end) : C-2201G16 (AC-AL132855)  
----- Summary Statistics  
Assembly program: Phrap, version 2.0  
Quality coverage: 7.94x in Q20 bases; sum-of-configs  
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Overall quality chart :  
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Range : bases  
0 - 9 :  
1 - 9 :  
10 - 19 :  
20 - 29 :  
30 - 39 :  
40 - 49 :  
50 - 59 :  
60 - 69 :  
70 - 79 :  
80 - 89 :  
90 - 99 :  
Percentage of bases with a quality value >= 40 : 99 %  
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RHdb:RH98727  
dbSTS:STS68485  
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## RESULT 14

AC079885 151212 bp DNA linear HTG 08-NOV-2000  
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 DEFINITION Norway, WORKING DRAFT SEQUENCE, 5 unordered pieces.  
 AC079885 2 GT:11120768  
 AC079885.2  
 VERSION HTG: HTGS\_PHASE1: HTGS\_DRAFT.  
 KEYWORDS Norway rat.  
 SOURCE Rattus norvegicus  
 ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

## REFERENCE

AUTHORS Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Gupta, J., Ho, S.-L., Idol, J., Karlins, E., Lee-Lin, S.-O., Legaspi, R., Lim, M., Maduro, Q.L., Maduro, V.B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Snyder, B., Stancir, P., Thomas, J.W., Thomas, P.J., Tjongson, E.E., Touchman, J.W., Tsurgou, C., Vogt, J.L., Walker, M.A., Wetherby, K.D. and Green, E.D.  
 TITLE NISC Mouse Sequencing Initiative  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 151212)  
 AUTHORS Green, E.D.

## COMMENT

Direct Submission  
 Submitted (16-SEP-2000) NIH Intramural Sequencing Center, 8717  
 Government Circle, Gaithersburg, MD 20877, USA  
 On Nov 8, 2000 this sequence version replaced g1:10179358.  
 Genome Center  
 Center: NIH Intramural Sequencing Center  
 Center code: NISC  
 Web site: http://www.nisc.nih.gov  
 Contact: nisc.mouse@nih.gov  
 Project Information  
 Center project name: rk  
 Center clone name: 246H18  
 Summary Statistics  
 Sequencing vector: plasmid; n/a; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 147800 bases at least Q40  
 Consensus quality: 149333 bases at least Q30  
 Consensus quality: 149333 bases at least Q20  
 Insert size: 145000; agarose-fp  
 Insert size: 150812; sum-of-coverage  
 Quality coverage: 11.76x in Q20 bases; agarose-fp

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 Quality coverage: 11.30x in Q20 bases; sum-of-coverage  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 5 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \* 1 20440: contig of 20440 bp in length  
 \* 20541 20540: gap of unknown length  
 \* 20541 41009: contig of 20469 bp in length  
 \* 41010 41009: gap of unknown length  
 \* 41110 65552: contig of 24443 bp in length  
 \* 65553 65552: gap of unknown length  
 \* 65653 110365: contig of 44713 bp in length  
 \* 110366 110465: gap of unknown length  
 \* 110466 151212: contig of 40747 bp in length.  
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 20541. 41009  
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 Db 74635 CTGATACACCAAGCATGGCTGCTGAGACAAATTAGAGACCCACTTCCAGACAC 74694  
 QY 181 tctctgacatcgtgagcagctgagatgagtcgagaccgcttcgcgcagc 240  
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 QY 241 caggtctccgacgaacttttcaaggaggcccaactgaggccgcttcgagccttc 300  
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Thu Jun 6 16:39:17 2002

us-09-155-327e-6.rge

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Page 12

Mouse bcl-*w* gene d  
Nucleotide sequenc  
Human secreted pro  
Human immune syste  
Human immune syste  
Human breast cell  
Human foetal liver  
Probe #10836 for g  
Human brain expres  
Human bone marrow  
Probe #10169 for g  
Probe #14164 used f  
Probe #5931 used t  
Rat wild-type Bcl-1  
Mutant bcl-*xl* codi  
cDNA clone HP03564  
Human thymus BCL-X  
Bcl-XL gene. Homo  
Bcl-*l* gene. Homo  
Human bcl-*l* cDNA.  
Human bcl-*xl* nucle  
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Base sequence of t  
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Lrh-Bcl-*xl* apoptos  
Human Bcl-*xl* (Iran  
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DNA encoding human  
Bcl-2. Homo sapie  
Bcl-2 DNA fragment  
Human oncogene bcl  
Human bcl-2 gene.  
Human bcl2 proto-o  
Human Bcl-2 protein  
Sequence of bcl-2  
Base sequence of t

DR WPI, 1997-489635/45.  
 DR P-PSDB; AAM36047.

PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce  
 PT or inhibit cell survival, e.g. for treatment of cancer and  
 PT degenerative diseases

XX Claim 3: Page 48; 86pp; English.

CC This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene  
 CC family, extracted from an adult brain library. This gene promotes cell  
 CC survival, so its modulation is useful in treatment of cancer or  
 CC auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's  
 CC disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia,  
 CC human immunodeficiency virus infection or in cell transplants,  
 CC UP-regulation of the gene can also be used to modify cell lines cultured  
 CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas  
 CC and to increase survival of primary explants during genetic modification.  
 CC It can be used to produce recombinant Bcl-w for therapy, diagnosis,  
 CC antibody production or screening of potential modulators.

CC Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other;

Query Match 99.2%; Score 578.2; DB 18; Length 583;  
 Best Local Similarity 99.5%; Pred. No. 3e-134;  
 Matches 580; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 atggcagccagcagcctggcccccagacacagcgcctgtgtgagacattttagttat 60  
 Db 1 atggcagccagcagcctggcccccagacacagcgcctgtgtgagacattttagttat 60  
 OY 61 aagctgaagcgaaggggtatgtctgtgagctggcccgaggagggcccaagctgac 120  
 Db 61 aagctgaagcgaaggggtatgtctgtgagctggcccgaggagggcccaagctgac 120  
 OY 121 ccgctgacacaaagcagctgagcagctgagatgagttcgaagccgctccggcgac 180  
 Db 121 ccgctgacacaaagcagctgagcagctgagatgagttcgaagccgctccggcgac 180  
 OY 181 ttctctgatctggcgtcagctgcatgtgacccagcagctcagccagcaacgcttcacc 240  
 Db 181 ttctctgatctggcgtcagctgcatgtgacccagcagctcagccagcaacgcttcacc 240  
 OY 241 caagctccagcagacattttcaaggggccccaactggggcgccctgttaacctttt 300  
 Db 241 caagctccagcagacattttcaaggggccccaactggggcgccctgttaacctttt 300  
 OY 301 gtctttggggtcgtcactgtgtctgagagtgtaacaagaagatggaaccactgtgga 360  
 Db 301 gtctttggggtcgtcactgtgtctgagagtgtaacaagaagatggaaccactgtgga 360  
 OY 361 caagctgcaagagtgatgtgtgctgacccctgagagcagcgctgctgactgataccagc 420  
 Db 361 caagctgcaagagtgatgtgtgctgacccctgagagcagcgctgctgactgataccagc 420  
 OY 421 agtggaggtcgtggcagagttcacagctctatacgggagcggccctggaggaagcgagg 480  
 Db 421 agtggaggtcgtggcagagttcacagctctatacgggagcggccctggaggaagcgagg 480  
 OY 481 cgtctgagcgaagggaggaactgagcagcagtgagagacagtcgagacggggccgtgacactg 540  
 Db 481 cgtctgagcgaagggaggaactgagcagcagtgagagacagtcgagacggggccgtgacactg 540  
 OY 541 ggggcctgtgaactgtaggggcttttttctgtagcaagttaa 583  
 Db 541 ggggcctgtgaactgtaggggcttttttctgtagcaagttaa 583

RESULT 2  
 AAX25134  
 ID AAX25134 standard; DNA; 583 BP.  
 XX

AC AAX25134;  
 XX  
 XX 05-JUL-1999 (first entry)  
 DR  
 DE Human bcl-w gene derivative.  
 XX  
 KW Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;  
 KW animal model; ss.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO9913710-A1.  
 XX  
 PD 25-MAR-1999.  
 XX  
 PF 16-SEP-1998; 98WO-AU00764.  
 XX  
 PR 16-SEP-1997; 97AU-0009228.  
 XX  
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
 XX  
 PI Adams J, Cory S, Gibson L, Koentgen F, Print C;  
 XX  
 DR WPI; 1999-243890/20.  
 DR P-PSDB; AAY05532.  
 XX  
 PT An animal model exhibiting reduced levels of a Bcl-w protein and/or  
 PT protein associated with Bcl-w  
 XX  
 PS Disclosure; Page 36; 52pp; English.

CC The present sequence is described as a derivative of the human  
 CC bcl-w gene (see AAX25132) and encodes Bcl-w protein (see AAY05532), a  
 CC pro-survival member of the Bcl-2 family which is widely expressed  
 CC and which is essential for spermatogenesis. The invention relates  
 CC generally to a method of treatment and to an animal model for the  
 CC identification of molecules and genetic sequences useful for  
 CC inducing or reducing fertility of male animals. Methods are  
 CC provided for the treatment of infertility, or for reducing  
 CC fertility, by modulating spermatogenesis. An animal model carries  
 CC a mutation in at least one allele of the human or murine bcl-w gene  
 CC or in a gene associated with bcl-w. Such animals have disorganised  
 CC seminiferous tubules and are substantially infertile, but possess no  
 CC other major abnormalities as determined by histological examination.  
 CC They can be used to screen for therapeutic molecules including  
 CC genetic sequences capable of inducing, enhancing or otherwise  
 CC facilitating spermatogenesis in animals, or which can induce  
 CC infertility.

CC Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other;

Query Match 99.2%; Score 578.2; DB 20; Length 583;  
 Best Local Similarity 99.5%; Pred. No. 3e-134;  
 Matches 580; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 atggcagccagcagcctggcccccagacacagcgcctgtgtgagacattttagttat 60  
 Db 1 atggcagccagcagcctggcccccagacacagcgcctgtgtgagacattttagttat 60  
 OY 61 aagctgaagcgaaggggtatgtctgtgagctggcccgaggagggcccaagcagctgac 120  
 Db 61 aagctgaagcgaaggggtatgtctgtgagctggcccgaggagggcccaagcagctgac 120  
 OY 121 ccgctgacacaaagcagctgagcagctgagatgagttcgaagccgctccggcgac 180  
 Db 121 ccgctgacacaaagcagctgagcagctgagatgagttcgaagccgctccggcgac 180  
 OY 181 ttctctgatctggcgtcagctgcatgtgaccccaagcagctcagccagcaacgcttcacc 240  
 Db 181 ttctctgatctggcgtcagctgcatgtgaccccaagcagctcagccagcaacgcttcacc 240  
 OY 241 caagctccagcagacattttcaaggggccccaactgaggcgccctgttagcttctt 300

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DB 241 caggtctccgacgaacttttcaagggggcccccaactggcgcccttgagcctctt 300
OY 301 gtcttggggctgcagctgtctgtagagtgtaacaagagatggaaccactggtagga 360
DB 301 cctcttggggctgcagctgtctgtagagtgtaacaagagatggaaccactggtagga 360
OY 361 caagtcgagggatgtagtgtagcttaactgtagacgcggctgctgtagctgtagcagc 420
DB 361 caagtcgagggatgtagtgtagcttaactgtagacgcggctgctgtagctgtagcagc 420
OY 421 agtggggctgtagcagctcacaagctctatacggggagcgccctggagggcgcg 480
DB 421 agtggggctgtagcagctcacaagctctatacggggagcgccctggagggcgcg 480
OY 481 cgtctcgaggaggaactgtagcacaatgtagcagtgtagcagggcgccctgtagcag 540
DB 481 cgtctcgaggaggaactgtagcacaatgtagcagtgtagcagggcgccctgtagcag 540
OY 541 ggggcccctgtaactgtaggggccccttttctagcaagtga 583
DB 541 ggggcccctgtaactgtaggggccccttttctagcaagtga 583

```

## RESULT 3

AAV25132 standard; DNA; 581 BP.

AAV25132:

05-JUL-1999 (first entry)

Human bcl-w gene.

Spermatogenesis: bcl-3 gene; Bcl-2; human; fertility; infertility;

animal model; ss.

Homo sapiens.

WO9913710-A1.

25-MAR-1999.

16-SEP-1998; 98WO-AU00764.

16-SEP-1997; 97AU-0009228.

(HALL-) HALL INST MEDICAL RES WALTER &amp; ELIZA.

Adams J, Cory S, Gibson L, Koentgen F, Print C;

WPI: 1999-243890/20.

P-PSDB: AAY05530.

An animal model exhibiting reduced levels of a Bcl-w protein and/or

protein associated with Bcl-w

Claim 3; Page 32; 52pp: English.

The present sequence is the human bcl-w gene encoding Bcl-w protein (see AAY05530), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method for treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene or in a gene associated with bcl-w. Such animals have disorganized seminiferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of

inducing, enhancing or otherwise facilitating spermatogenesis in CC animals, or which can induce infertility.

Sequence 581 BP; 104 A; 155 C; 210 G; 112 T; 0 other;

Query Match 99.1%; Score 577.8; DB 20; Length 581;  
Best Local Similarity 99.7%; Pred. No. 3.7e-134;  
Matches 579; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY 1 atgagcaccacagcctcgccccaagacacagggctctgtgtagcagattgagttat 60
DB 1 atgagcaccacagcctcgccccaagacacagggctctgtgtagcagattgagttat 60
OY 61 aagctgagcagaaaggtatgtctgtgtagcctgcccggggagggccagcagctgac 120
DB 61 aagctgagcagaaaggtatgtctgtgtagcctgcccggggagggccagcagctgac 120
OY 121 ccgctgacacacagcctcgccccaagcctgtagatgagttgtagaccgctcccgagc 180
DB 121 ccgctgacacacagcctcgccccaagcctgtagatgagttgtagaccgctcccgagc 180
OY 181 tctctgacatcgccgctcagctgtagctgtagcctcagccagcctcagccagcctcacc 240
DB 181 tctctgacatcgccgctcagctgtagctgtagcctcagccagcctcagccagcctcacc 240
OY 241 caagctccgacgaacttttcaaggggcccccaactggggcgccctgtgagcctctt 300
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OY 301 gtcttggggctgcagctgtctgtagagtgtaacaagagatggaaccactggtagga 360
DB 301 gtcttggggctgcagctgtctgtagagtgtaacaagagatggaaccactggtagga 360
OY 361 caagtcgagggatgtagtgtagcttaactgtagacgcggctgctgtagctgtagcagc 420
DB 361 caagtcgagggatgtagtgtagcttaactgtagacgcggctgctgtagctgtagcagc 420
OY 421 agtggggctgtagcagctcacaagctctatacggggagcgccctggagggcgcg 480
DB 421 agtggggctgtagcagctcacaagctctatacggggagcgccctggagggcgcg 480
OY 481 cgtctcgaggaggaactgtagcacaatgtagcagtgtagcagggcgccctgtagcag 540
DB 481 cgtctcgaggaggaactgtagcacaatgtagcagtgtagcagggcgccctgtagcag 540
OY 541 ggggcccctgtaactgtaggggccccttttctagcaagtga 581
DB 541 ggggcccctgtaactgtaggggccccttttctagcaagtga 581

```

## RESULT 4

AAV28334 standard; cDNA; 579 BP.

AAV28334:

02-OCT-1998 (first entry)

Human bcl-y gene.

ss: bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.

Homo sapiens.

Key Location/Qualifiers

FT CDS 1..579

FT /product= bcl-y

FT /note= "No stop codon given"

XX

XX

PD 04-AUG-1998.  
 XX  
 PF 11-FEB-1997; 97US-0798897.  
 XX  
 PR 23-FEB-1996; 96US-0012201.  
 PR 11-FEB-1997; 97US-0798897.  
 XX  
 PA (COCE-) COCENSYS INC.  
 XX  
 PI Guastella J;  
 XX  
 DR WPI: 1998-446079/38.  
 XX P-PSDB; AAM61392.  
 XX  
 PT Nucleic acids encoding B-cell lymphoma-Y protein - useful for  
 PT producing recombinant protein for use in treating uncontrolled cell  
 PS growth e.g. cancers  
 XX  
 PS Claim 3; Column 15/16; 27pp; English.  
 CC The mammalian bcl-y genes encode a protein that is a member of the bcl-2  
 CC family, components in the cell death pathway. The bcl-2 family  
 CC have both apoptotic activity and the apoptosis blocking activity. bcl-y  
 CC falls in the apoptosis activity category. The recombinant protein may  
 CC be used to prevent uncontrolled cell growth, either by its direct  
 CC administration to recombinant genetic constructs to increase its  
 CC expression in vivo. Also, antisense constructs can be used in disorders  
 CC where prevention of cell death is desired.  
 XX  
 SQ Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;

Query Match 98.2%; Score 572.6; DB 19; Length 579;  
 Best Local Similarity 99.3%; Pred. No. 7.2e-133;  
 Matches 575; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 atgggacccagcctcgccacacacagggcctctgtgcaagactttagttat 60  
 DB 1 atgggacccagcctcgccacacacagggcctctgtgcaagactttagttat 60  
 QY 61 aagctgagcagaaggtatgtctgtgagctgagcccgaggagggccagcagctgac 120  
 DB 61 aagctgagcagaaggtatgtctgtgagctgagcccgaggagggccagcagctgac 120  
 QY 121 ccgctgacacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180  
 DB 121 ccgctgacacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180  
 QY 181 ttctctgacatgctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 240  
 DB 181 ttctctgacatgctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 240  
 QY 241 caagttccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300  
 DB 241 caagttccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300  
 QY 301 gtctctgagcctgacagctgtgtgtgagtgatgtaacaagaatggaacacactgtgtgga 360  
 DB 301 gtctctgagcctgacagctgtgtgtgagtgatgtaacaagaatggaacacactgtgtgga 360  
 QY 361 caagttcagaagtgatgagtgagcctgagcagcagcagcagcagcagcagcagcagcagcagc 420  
 DB 361 caagttcagaagtgatgagtgagcctgagcagcagcagcagcagcagcagcagcagcagcagc 420  
 QY 421 agtgggggctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480  
 DB 421 agtgggggctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480  
 QY 481 cgtctcgaggagggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 540  
 DB 481 cgtctcgaggagggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 540  
 QY 541 gggggcctgtgtaactgtagggccttttctgtagcaag 579

DB 541 gggggcctgtgtaactgtagggccttttctgtagcaag 579

RESULT 5  
 ID AAX15946  
 AAX15946 standard; CDNA; 579 BP.

AAX15946;

20-MAY-1999 (first entry)

CDNA encoding the human bcl-y protein.

Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;  
 programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
 head trauma; Alzheimer's disease; neural; muscular degenerative disease;  
 multiple sclerosis; myocardial infarction; vitally induced cell death;  
 aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
 premature cell death; cell death stimulator; prolonged cell life span;  
 Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;  
 parasite; ss.

Homo sapiens.

US5883229-A.

16-MAR-1999.

25-NOV-1997; 97US-0978523.

23-FEB-1996; 96US-0012201.

11-FEB-1997; 97US-0798897.

25-NOV-1997; 97US-0978523.

(COCE-) COCENSYS INC.

Guastella J;

WPI: 1999-214150/18.

P-PSDB; AAM97392.

Novel bcl-y homologues of the rat and human bcl-2 protein - useful  
 for modulating programmed cell death

Disclosure; Columns 15-16; 26pp; English.

The present sequence encodes human bcl-y protein (Hbcl-y). The  
 specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and  
 Hbcl-y are homologues of the bcl-2 protein thought to be involved in  
 programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y  
 proteins may be used to treat conditions associated with a disruption of  
 the cell death pathway. If they act as cell death inhibitors, they may be  
 used in therapies to treat subjects suffering from: strokes, head trauma,  
 Alzheimer's disease, neural and muscular degenerative diseases  
 (especially multiple sclerosis), myocardial infarction, vitally induced  
 cell death, aging, spinal cord injuries and amyotrophic lateral  
 sclerosis - conditions where cells under go premature cell death as a  
 result of triggers which may or may not be apparent. They may also be  
 used in this way to develop cell lines which remain viable in culture for  
 an extended period. In contrast, if they act as cell death stimulators,  
 Rbcl-y and Hbcl-y may be used to treat conditions associated with  
 prolonged cell life span such as cancer (especially Kaposi's sarcoma and  
 lung cancer) and auto/hyperimmune diseases. They may also be used to  
 cause cell death in, and hence control, parasites.

Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;

Query Match 98.2%; Score 572.6; DB 20; Length 579;  
 Best Local Similarity 99.3%; Pred. No. 7.2e-133;  
 Matches 575; Conservative 0; Mismatches 4; Indels 0; Gaps 0;



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   |||
Db 1 atgagcagcccccagctcgcccccagacacagcgcctcgtgtgagagactttagatgta 60
OY 61 aagctgagcagaaagagatgctcgtgagctgccccggggggggccagcagctgac 120
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   |||
   |||
Db 61 aagctgagcagaaagagatgctcgtgagctgccccggggggggccagcagctgac 120
OY 121 ccgctgcacacagcagctcgccagctgagatgattcggagaccggcttcggcgacac 180
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Db 121 ccagctgcacacagcagctcgccagctgagatgattcggagaccggcttcggcgacac 180
OY 181 ttctctgagctcgagctgagctgagctgagctgagctgagctgagctgagctgagc 240
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Db 361 caagctgagagatgagatgagctgagctgagcagcagctgagctgagctgagctgagc 420
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Db 421 agtgggggctgagcagctgagctgagctgagctgagctgagctgagctgagctgagc 480
OY 481 cgtctcgagaggggagaaactgggcatcagtgagagcagtgctgagcggggcgctggcagc 540
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Db 481 cgtctcgagaggggagaaactgggcatcagtgagagcagtgctgagcggggcgctggcagc 540
OY 541 ggggcccctggttaactgtgaggggctttttgctagcaag 579
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Db 541 ggggcccctggttaactgtgaggggctttttgctagcaag 579

RESULT 6
AAV28333 standard: CDNA: 579 BP.
ID AAV28333:
XX
AC AAV28333:
XX
DT 02-OCT-1998 (first entry)
XX
DE Rat bcl-y gene.
XX
KW ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
XX
XX Ratius sp.
XX
OS
XX
FH Key Location/Qualifiers
FT CDS 1..579
FT /tag= a
FT /product= bcl-y
FT /note="No stop codon given"
XX
XX US5789201-A.
XX
XX PD 04-AUG-1998.
XX
XX PF 11-FEB-1997; 97US-0798897.
XX
XX PR 23-FEB-1996; 96US-0012201.
XX
XX PR 11-FEB-1997; 97US-0798897.
XX
XX PA (COCE-) COCENSYS INC.
XX
XX PT Guastella J;
```

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XX
DR WPI: 1998-446079/38.
DR P-PSDB: AAM61391.
XX
XX Nucleic acids encoding B-cell lymphoma-Y protein - useful for
PT producing recombinant protein for use in treating uncontrolled cell
PT growth e.g. cancers
XX
XX Claim 2: Column 13/14; 27pp; English.
XX
XX The mammalian bcl-y genes encode a protein that is a member of the bcl-2
XX family, components in the cell death pathway. The bcl-2 family
XX have both apoptotic activity and the apoptosis blocking activity. bcl-y
XX falls in the apoptosis activity category. The recombinant protein may
XX be used to prevent uncontrolled cell growth, either by its direct
XX administration to recombinant genetic constructs to increase its
XX expression in vivo. Also, antisense constructs can be used in disorders
XX where prevention of cell death is desired.
XX
XX Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 other;
XX
XX
XX Query Match 90.5%; Score 527.8; DB 19; Length 579;
XX Best Local Similarity 94.5%; Pred. No. 9, 6e-122;
XX Matches 547; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
OY 1 atgagcagcccccagctcgcccccagacacagcgcctcgtgtgagagactttagatgta 60
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Db 1 atgagcagcccccagctcgcccccagacacagcgcctcgtgtgagagactttagatgta 60
OY 61 aagctgagcagaaagagatgctcgtgagctgccccggggggggccagcagctgac 120
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   |||
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Db 61 aagctgagcagaaagagatgctcgtgagctgccccggggggggggccagcagctgac 120
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OY 181 ttctctgagctcgagctgagctgagctgagctgagctgagctgagctgagctgagc 240
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Db 181 ttctctgagctcgagctgagctgagctgagctgagctgagctgagctgagctgagc 240
OY 241 caagctcgcagcagactttttcaagggggggcccaactggcgccgcttgtagcttctt 300
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Db 241 caagctcgcagcagactttttcaagggggggggcccaactggcgccgcttgtagcttctt 300
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Db 301 gtctttgggctgctgactgtgtgctgagagtgatcaacaagagatgagacactgtgag 360
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OY 421 agtgggggctgagcagctgagctgagctgagctgagctgagctgagctgagctgagc 480
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Db 421 agtgggggctgagcagctgagctgagctgagctgagctgagctgagctgagctgagc 480
OY 481 cgtctcgagaggggagaaactgggcatcagtgagagcagtgctgagcggggcgctggcagc 540
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Db 481 cgtctcgagaggggagaaactgggcatcagtgagagcagtgctgagcggggcgctggcagc 540
OY 541 ggggcccctggttaactgtgaggggctttttgctagcaag 579
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Db 541 ggggcccctggttaactgtgaggggctttttgctagcaag 579

RESULT 7
AAV15945 standard: CDNA: 579 BP.
ID AAV15945:
XX
AC AAV15945:
XX
DT 02-OCT-1998 (first entry)
XX
DE Rat bcl-y gene.
XX
KW ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
XX
XX Ratius sp.
XX
OS
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FH Key Location/Qualifiers
FT CDS 1..579
FT /tag= a
FT /product= bcl-y
FT /note="No stop codon given"
XX
XX US5789201-A.
XX
XX PD 04-AUG-1998.
XX
XX PF 11-FEB-1997; 97US-0798897.
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XX PR 23-FEB-1996; 96US-0012201.
XX
XX PR 11-FEB-1997; 97US-0798897.
XX
XX PA (COCE-) COCENSYS INC.
XX
XX PT Guastella J;
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20-MAY-1999 (first entry)  
 XX XX  
 DE cDNA encoding the rat bcl-1 protein.  
 XX XX  
 KW Rat bcl-1 protein; Rbcl-1; human bcl-1 protein; Hbcl-1; bcl-2 homologues;  
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
 KW head trauma; Alzheimer's disease; neural; muscular degenerative disease;  
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;  
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
 KW premature cell death; cell death stimulator; prolonged cell life span;  
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;  
 KW parasite; ss.  
 XX XX  
 OS Rattus sp.  
 XX XX  
 PN US5883229-A.  
 XX XX  
 PD 16-MAR-1999.  
 XX XX  
 PF 25-NOV-1997; 97US-0978523.  
 XX XX  
 PR 23-FEB-1996; 96US-0012201.  
 PR 11-FEB-1997; 97US-0798897.  
 PR 25-NOV-1997; 97US-0978523.  
 XX XX  
 PA (COCE-) COCENSYS INC.  
 XX XX  
 PI Guastella J;  
 XX XX  
 DR WPI; 1999-214150/18.  
 DR P-PSDB; AAW97391.  
 XX XX  
 PT Novel bcl-1 homologues of the rat and human bcl-2 protein - useful  
 PT for modulating programmed cell death  
 XX XX  
 PS Disclosure; Columns 13-16; 26pp; English.  
 XX XX  
 CC The present sequence encodes rat bcl-1 protein (Rbcl-1). The  
 CC specification also describes human bcl-1 protein (Hbcl-1). Rbcl-1 and  
 CC Hbcl-1 are homologues of the bcl-2 protein thought to be involved in  
 CC programmed cell death (apoptosis and necrosis). Rbcl-1 and Hbcl-1  
 CC proteins may be used to treat conditions associated with a disruption of  
 CC the cell death pathway. If they act as cell death inhibitors, they may be  
 CC used in therapies to treat subjects suffering from: strokes, head trauma,  
 CC Alzheimer's disease, neural and muscular degenerative diseases  
 CC (especially multiple sclerosis), myocardial infarction, vitally induced  
 CC cell death, aging, spinal cord injuries and amyotrophic lateral  
 CC sclerosis- conditions where cells under go premature cell death as a  
 CC result of triggers which may or may not be apparent. They may also be  
 CC used in this way to develop cell lines which remain viable in culture for  
 CC an extended period. In contrast, if they act as cell death stimulators,  
 CC Rbcl-1 and Hbcl-1 may be used to treat conditions associated with  
 CC prolonged cell life span such as cancer (especially Kaposi's sarcoma and  
 CC lung cancer) and auto/hyperimmune diseases. They may also be used to  
 CC cause cell death in, and hence control, parasites.  
 XX XX  
 SQ Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 other;

Query Match 90.5%; Score 527.8; DB 20; Length 579;  
 Best Local Similarity 94.5%; Pred. No. 9.6e-122;  
 Matches 547; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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 QY 61 aagctgagcagagaggttatgtctgtgagctggcccgaggagggccagagcttgaac 120  
 Db 61 aagctgagcagagaggttatgtctgtgagctggcccgaggagggccagagcttgaac 120  
 QY 121 ccgctgcacacagcattcgaggagctgagatgagttcagagccgcttcggcgacac 180  
 Db 121 ccgctgcacacagcattcgaggagctgagatgagttcagagccgcttcggcgacac 180

Db 121 ccgctgcacacagcattcgaggagctgagatgagttcagagccgcttcggcgacac 180  
 QY 181 ttctctgacatggcgagctgaagctgacatgtgacccagagctcagccagcgttcac 240  
 Db 181 ttctctgacatggcgagctgaagctgacatgtgacccagagctcagccagcgttcac 240  
 QY 241 caagctccagagacattttcaagaggggccccaacttggggccgcttgaagcttc 300  
 Db 241 caagctccagagacattttcaagaggggccccaacttggggccgcttgaagcttc 300  
 QY 301 gctcttggggctgcaacttctgtctgagagtgtaacaagagatcagacacagctgg 360  
 Db 301 gctcttggggctgcaacttctgtctgagagtgtaacaagagatcagacacagctgg 360  
 QY 361 caagtgacagagatgtgctgcttaccatgagacggcgctgctgacatgacacagc 420  
 Db 361 caagtgacagagatgtgctgcttaccatgagacggcgctgctgacatgacacagc 420  
 QY 421 agtggggctgagcggagttcacagctctatacggagacggggccctgagagggcg 480  
 Db 421 agtggggctgagcggagttcacagctctatacggagacggggccctgagagggcg 480  
 QY 481 cgtctcgaggaggaggaactgggacatcagtgagagacagtgctcagggggcgctg 540  
 Db 481 cgtctcgaggaggaggaactgggacatcagtgagagacagtgctcagggggcgctg 540  
 QY 541 ggggcccctgtaactcagagtgagggccttttctgacagcaag 579  
 Db 541 ggggcccctgtaactcagagtgagggccttttctgacagcaag 579

RESULT 8  
 AAX25133  
 ID AAX25133 standard; DNA; 581 BP.  
 XX XX  
 AC AAX25133;  
 XX XX  
 DT 05-JUL-1999 (first entry)  
 XX XX  
 DE Mouse bcl-1 gene.  
 XX XX  
 KW Spermatogenesis; bcl-1 gene; Bcl-2; mouse; fertility; infertility;  
 KW animal model; ss.  
 XX XX  
 OS Mus sp.  
 XX XX  
 PN MO9913710-A1.  
 XX XX  
 PD 25-MAR-1999.  
 XX XX  
 PF 16-SEP-1998; 98WO-AU00764.  
 XX XX  
 PR 16-SEP-1997; 97AU-0009228.  
 XX XX  
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
 XX XX  
 PI Adams J, Cory S, Gibson L, Koentgen F, Print C;  
 XX XX  
 DR WPI; 1999-243890/20.  
 XX XX  
 PR P-PSDB; AAY05531.  
 XX XX  
 PT An animal model exhibiting reduced levels of a Bcl-1 protein and/or  
 PT protein associated with Bcl-1  
 XX XX  
 PS Claim 3; Page 34; 52pp; English.  
 XX XX

The present sequence is the mouse bcl-1 gene encoding Bcl-1 protein  
 (see AAY05531), a pro-survival member of the Bcl-2 family which is  
 widely expressed and which is essential for spermatogenesis. The  
 invention relates generally to a method of treatment and to an  
 animal model for the identification of molecules and genetic  
 sequences useful for inducing or reducing fertility of male  
 animals. Methods are provided for the treatment of infertility, or

for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene or in a gene associated with bcl-w. Such animals have disorganised seminiferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility.

Sequence 581 BP; 106 A; 158 C; 200 G; 117 T; 0 other:

Query Match 90.3%; Score 526.6; DB 20; Length 581;  
Best Local Similarity 94.1%; Pred. No. 1.9e-121;  
Matches 547; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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Db 1 atggcagcccccagcctcgcgcacacacagcgcctctgtgtggaagctttagttagt 60
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    |||||||
Db 61 aagctgagcaggaaggtatgtctgtgagctgcccggggaagcagcagctgac 120
QY 121 ccgctgcacacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
    |||||||
Db 121 ccgctgcacacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
QY 181 ttctctgacatgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 240
    |||||||
Db 181 ttctctgacatgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 240
QY 241 caagctccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300
    |||||||
Db 241 caagctccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300
QY 301 gctcttgaggcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 360
    |||||||
Db 301 gctcttgaggcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 360
QY 361 caagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 420
    |||||||
Db 361 caagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 420
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    |||||||
Db 421 agtggggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480
QY 481 cgtctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 540
    |||||||
Db 481 cgtctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 540
QY 541 ggggcccctgtactgttagggccttttctgttagcaagt 581
    |||||||
Db 541 ggggcccctgtactgttagggccttttctgttagcaagt 581

```

RESULT 9  
AKI96578  
ID AAT96578 standard; DNA; 581 BP.  
AC AAT96578;  
XX 22-APR-1998 (first entry)  
XX  
XX Mouse bcl-w DNA.  
XX Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;  
XX diagnosis; degenerative disease; ss.  
XX  
XX Mus sp.  
XX

FH Key Location/Qualifiers  
FT CDS 1..507  
FT /\*tag= a  
FT /product= bcl-w  
FT /note= "q"  
XX  
XX WO9735971-A1.  
XX 02-OCT-1997.  
XX  
XX 27-MAR-1997; 97WO-AU00199.  
XX  
XX 27-MAR-1996; 96AU-0008965.  
XX  
XX (AMRA-) AMRAD OPERATIONS PTY LTD.  
XX Adams JM, Cory S, Gibson LM, Holmgreen SP;  
XX P-PSDB; AAW36048.  
XX WPI: 1997-489635/45.  
XX  
XX Nucleic acid encoding apoptosis related gene bcl-w - used to induce  
XX or inhibit cell survival, e.g. for treatment of cancer and  
XX degenerative diseases  
XX  
XX Claim 3; Page 50-51; 86pp; English.  
XX  
XX This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene  
XX family. This gene promotes cell survival, so its modulation is useful in  
XX treatment of cancer or auto-immune diseases, degenerative diseases (e.g.  
XX stroke, Alzheimer's disease, myocardial infarct, muscular degeneration,  
XX hypoxia, ischaemia, human immunodeficiency virus infection or in cell  
XX transplants. Up-regulation of the gene can also be used to modify cell  
XX lines cultured in vivo, e.g. to develop new lines, to facilitate  
XX isolation of hybridomas and to increase survival of primary explants  
XX during genetic modification. It can be used to produce recombinant bcl-w  
XX for therapy, diagnosis, antibody production or screening of potential  
XX modulators.  
XX  
XX Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 other:

Query Match 86.8%; Score 505.8; DB 18; Length 581;  
Best Local Similarity 91.9%; Pred. No. 2.8e-116;  
Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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Db 1 atggcagcccccagcctcgcgcacacacagcgcctctgtgtggaagctttagttagt 60
QY 61 aagctgagcaggaaggtatgtctgtgagctgcccggggaagcagcagctgac 120
    |||||||
Db 61 aagctgagcaggaaggtatgtctgtgagctgcccggggaagcagcagctgac 120
QY 121 ccgctgcacacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
    |||||||
Db 121 ccgctgcacacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
QY 181 ttctctgacatgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 240
    |||||||
Db 181 ttctctgacatgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 240
QY 241 caagctccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300
    |||||||
Db 241 caagctccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300
QY 301 gctcttgaggcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 360
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Db 301 gctcttgaggcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 360
QY 361 caagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 420
    |||||||
Db 361 caagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 420

```

QY 421 agtgggagctggcggaattcacaagctctatacgggagcgccctggagagcgcg 480  
 DB 421 agtggcgagctggcggaattcacaagctctatacgggagcgccctggagagcgcg 480  
 QY 481 gcttcgagggaggggaactgggcatcagtagagagagctgtcagggcgctggcactg 540  
 DB 481 gcttcgagggaggggaactgggcatcagtagagagagctgtcagggcgctggcactg 540  
 QY 541 ggggcccctgttaactgtagggcgcttttctgctagcaactg 581  
 DB 541 ggggcccctgttaactgtagggcgcttttctgctagcaactg 581

## RESULT 10

AAK25135  
 ID AAK25135 standard; DNA; 581 BP.

AC AAK25135;

DT 05-JUL-1999 (first entry)

DE Mouse bcl-w gene derivative.

KW Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;  
 animal model; ss.

OS Mus sp.

FH Key Location/Qualifiers  
 FT CDS 1.507  
 ET /\*tag= a

PN W09913710-A1.

PD 25-MAR-1999.

PF 16-SEP-1998; 98WO-AU00764.

PR 16-SEP-1997; 97AU-0009228.

PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

PI Adams J, Cory S, Gibson L, Koentgen F, Print C;  
 DR WPI: 1999-243890/20.  
 DR P-PSDB; AAY05533.

PT An animal model exhibiting reduced levels of a Bcl-w protein and/or  
 protein associated with Bcl-w  
 PS Disclosure: Page 38; 52pp; English.

CC The present sequence is described as a derivative of the mouse  
 CC bcl-w gene (see AAK25133) and encodes Bcl-w protein (see AAY05533), a  
 CC pro-survival member of the Bcl-2 family which is widely expressed  
 CC and which is essential for spermatogenesis. The invention relates  
 CC generally to a method of treatment and to an animal model for the  
 CC identification of molecules and genetic sequences useful for the  
 CC inducing or reducing fertility of male animals. Methods are  
 CC provided for the treatment of infertility, or for reducing  
 CC fertility, by modulating spermatogenesis. An animal model carries  
 CC a mutation in at least one allele of the human or murine bcl-w gene  
 CC or in a gene associated with bcl-w. Such animals have disorganised  
 CC seminiferous tubules and are substantially infertile, but possess no  
 CC other major abnormalities as determined by histological examination.  
 CC They can be used to screen for therapeutic molecules including  
 CC genetic sequences capable of inducing, enhancing or otherwise  
 CC facilitating spermatogenesis in animals, or which can induce  
 CC infertility.

CC Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 other;

Query Match Best Local Similarity 86.8%; Score 505.8; DB 20; Length 581;  
 Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 atggcgagcccgagcctcgcccgagacacacgagcctgtgtgacagcttgaagttat 60  
 DB 1 atggcgagcccgagcctcgcccgagacacacgagcctgtgtgacagcttgaagttat 60  
 QY 61 aagctgagagcagaggggttatgtctgtgagcctgagcccgagggagcccaagctaac 120  
 DB 61 aagctgagagcagaggggttatgtctgtgagcctgagcccgagggagcccaagctaac 120  
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 DB 241 caagctcgcagagacattttcaagggggcccacactggggcgcttgaagcttctt 300  
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 QY 361 caagtcagagagtgatgtgtgagcagcagcagcagcagcagcagcagcagcagc 420  
 DB 361 caagtcagagagtgatgtgtgagcagcagcagcagcagcagcagcagcagcagc 420  
 QY 421 agtgggagctggcggaattcacaagctctatacgggagcgccctggagagcgcg 480  
 DB 421 agtgggagctggcggaattcacaagctctatacgggagcgccctggagagcgcg 480  
 QY 481 gcttcgagggaggggaactgggcatcagtagagagagctgtcagggcgctggcactg 540  
 DB 481 gcttcgagggaggggaactgggcatcagtagagagagctgtcagggcgctggcactg 540  
 QY 541 ggggcccctgttaactgtagggcgcttttctgctagcaactg 581  
 DB 541 ggggcccctgttaactgtagggcgcttttctgctagcaactg 581

## RESULT 11

AAV41925  
 ID AAV41925 standard; cDNA; 1098 BP.

AC AAV41925;

DT 20-MOV-1998 (first entry)

DE Nucleotide sequence of the cDNA clone Bcl-1 like (HATCH29).

KW Bcl-1 like (HATCH29); chronic inflammatory disease; allergic reaction;  
 immunological disorder; autoimmune disease; anti-infectious agent; ss.

OS Homo sapiens.

FH Key Location/Qualifiers  
 FT CDS 1..1098  
 ET /\*tag= a  
 FT /\*product= "Bcl-1 like (HATCH29) protein"

PN W09831800-A2.

PD 23-JUL-1998.

PF 21-JAN-1998; 98WO-US00960.

PR 21-JAN-1997; 97US-0034205.

XX 21-JAN-1997; 97US-0034204.  
XX (AUCK-) AUCKLAND UNISERVICES LTD.  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX Feng P, Gentz RL, Krissansen GW, NI J, Rosen CA:  
PI Su JY;  
XX WPI; 1998-41409/35.  
DR P-PSDB; AAW59884.  
XX  
XX New isolated polynucleotides and encoded polypeptides - used to  
PT develop products for treating e.g. inflammatory diseases, allergies  
PT infections, immunological disorders, autoimmune diseases, or tumours  
PT or tumours  
PS Claim 2; Fig 12A-12D; 120pp; English.  
XX  
XX This is the nucleotide sequence of the cDNA clone Bcl-like (HAICH29),  
CC used in the method of the invention. The products of the clone can be  
CC used for treating conditions associated with abnormal expression of  
CC the polypeptides. They can be used for e.g. treating chronic  
CC inflammatory diseases, immunological disorders, autoimmune diseases,  
CC inflammatory diseases, various allergies, and as anti-infectious agents.  
CC The products can also be used for detection and diagnosis.  
XX  
XX Sequence 1098 BP; 264 A; 279 C; 325 G; 230 T; 0 other;

Query Match 73.6%; Score 428.8; DB 19; Length 1098;  
Best Local Similarity 99.5%; Pred. No. 4; 2e-97;  
Matches 430; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 12  
AAV59630 standard; DNA; 1864 BP.  
ID AAV59630:  
XX AAV59630:  
AC AAV59630:  
XX 19-JAN-1999 (first entry)  
DT

XX Human secreted protein gene 120 clone HGB5264.  
XX  
XX Human: secreted protein; fusion protein; gene therapy; protein therapy;  
XX diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
XX developmental abnormality; foetal deficiency; blood; allergy; renal; ds;  
XX immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
XX inflammation; ischaemic shock; Alzheimer's disease; osteoclast; thymus;  
XX cognitive disorder; schizophrenia; prostate; obesity; thyroid; digestion;  
XX endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
XX  
XX Homo sapiens.  
XX  
XX W09839448-A2.  
XX  
XX 11-SEP-1998.  
XX  
XX 06-MAR-1998; 98WO-0504493.  
XX  
XX 02-OCT-1997; 97US-0061060.  
XX 07-MAR-1997; 97US-0038621.  
XX 07-MAR-1997; 97US-0040161.  
XX 07-MAR-1997; 97US-0040162.  
XX 07-MAR-1997; 97US-0040163.  
XX 07-MAR-1997; 97US-0040334.  
XX 07-MAR-1997; 97US-0040336.  
XX 07-MAR-1997; 97US-0040626.  
XX 11-APR-1997; 97US-0043311.  
XX 11-APR-1997; 97US-0043312.  
XX 11-APR-1997; 97US-0043313.  
XX 11-APR-1997; 97US-0043314.  
XX 11-APR-1997; 97US-0043568.  
XX 11-APR-1997; 97US-0043569.  
XX 11-APR-1997; 97US-0043570.  
XX 11-APR-1997; 97US-0043571.  
XX 11-APR-1997; 97US-0043572.  
XX 11-APR-1997; 97US-0043574.  
XX 11-APR-1997; 97US-0043576.  
XX 11-APR-1997; 97US-0043578.  
XX 11-APR-1997; 97US-0043580.  
XX 11-APR-1997; 97US-0043582.  
XX 11-APR-1997; 97US-0043584.  
XX 11-APR-1997; 97US-0043585.  
XX 11-APR-1997; 97US-0043586.  
XX 11-APR-1997; 97US-0043587.  
XX 11-APR-1997; 97US-0043588.  
XX 11-APR-1997; 97US-0043589.  
XX 11-APR-1997; 97US-0043590.  
XX 11-APR-1997; 97US-0043592.  
XX 11-APR-1997; 97US-0043594.  
XX 11-APR-1997; 97US-0043595.  
XX 11-APR-1997; 97US-0043596.  
XX 11-APR-1997; 97US-0043597.  
XX 11-APR-1997; 97US-0043598.  
XX 11-APR-1997; 97US-0043599.  
XX 11-APR-1997; 97US-0043600.  
XX 11-APR-1997; 97US-0043601.  
XX 11-APR-1997; 97US-0043612.  
XX 11-APR-1997; 97US-0043613.  
XX 11-APR-1997; 97US-0043614.  
XX 11-APR-1997; 97US-0043615.  
XX 11-APR-1997; 97US-0043617.

This sequence represents a nucleic acid molecule designated Gene 120 from the human cDNA clone HCBG2.64 (deposited as clone ATCC 97902 and ATCC 209048) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g., AAV5502) for increasing the stability of the fusion protein as compared to the human protein only. The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV5511-V59812; amino acid sequences AAW74731-W75026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological

1987, 2002MO-EF0/33/.

PR 30-JUN-2000; 2000DE-1032529.  
 PR 01-SEP-2000; 2000DE-1043826.  
 XX  
 PA (EPiG-) EPIGENOMICS AG.  
 PI Olek A, Piepenbrock C, Berlin K;  
 DR WPI; 2002-130909/17.

XX Nucleic acid comprising fragment of chemically modified gene, useful  
 PT for diagnosis and treatment of diseases associated with abnormal  
 PT cytosine methylation -

PS Claim 1; SEQ ID NO 201; 32pp + Sequence Listing; German.

XX The present invention provides a number of human immune system associated  
 CC genes which are modified by the methylation of cytosines. The sequences  
 CC can be used in the diagnosis and treatment of immune system disorders,  
 CC including eye diseases such as retinopathy, neovascular glaucoma and  
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid  
 CC leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel  
 CC diseases. The present sequence is a gene of the invention.

XX Sequence 6049 BP; 1480 A; 109 C; 1549 G; 2911 T; 0 other;

Query Match 44.1%; Score 257; DB 24; Length 6049;  
 Best Local Similarity 74.6%; Pred. No. 2,8e-54;  
 Matches 323; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

QY 1 atggagacccagcagctggccacacagcggcgtctgtgacagctttagtatt 60  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 5001 atggcagatttagtctggtttagatatacgggttctgtgtgtagatttgaagtatt 5060  
 QY 61 aagctggagcagaggtatgtctgtgagctggcccgaggagggccagcagctgac 120  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 5061 aagctggagcagaggtatgtctgtgagctggcccgaggaggggttagtagtatt 5120  
 QY 121 ccgctgacacagcagctgagcagctgagatgagctgagaccgcttcgagcagc 180  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 5121 tctgtgatttagatgagctgagctgagatgagctgagcttcgcttcgagctatt 5180  
 QY 181 ttcctatcggcggcgtcagctgacatgacacccagcagccacccagcagctcacc 240  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 5181 tttctgattcggcggcgtcagctgacatgacatgacatttagttataacgtttatt 5240  
 QY 241 caggtctcgcagcagcttttcaagggggcccaactggggcgccgttgagcctctt 300  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 5241 taggtttcagtgatatttttaagggggttttaattgggggtcgttttgagttttt 5300  
 QY 301 gttcttggcgtcagctgtgtgtcgtgagagtgtaacaaggagagatgacactgtgga 360  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 5301 gttttggggttgatctgtgtcgtgagagtgtaacaaggagagatgacactgtgga 5360  
 QY 361 caagtgcagagtgatgtgctacactgagagacggcgtcgtcagctgacacagc 420  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 5361 taagtgtcagagtgatgtgctacactgagagacggcgtcgtcagctgacacagc 5420  
 QY 421 agtggggcgagg 433  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 5421 agtggggcgagg 5433

RESULT 14  
 ABL32229/c  
 ID ABL32229 standard; DNA: 6049 BP.

XX ABL32229;  
 AC 26-MAR-2002 (first entry)  
 XX Human immune system associated gene SEQ ID NO: 202.  
 DE

XX Human; immune system disease; cytosine methylation; antiasthmatic;  
 KW antiarteriosclerotic; antianemic; cytosinic; nontropic;  
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;  
 KW antineuritic; antiarthritic; antidiabetic; antipsoriatic;  
 KW antineuritic; cancer; eye disease; arteriosclerosis; anaemia;  
 KW acute myeloid leukemia; Alzheimer's disease; AIDS; epilepsy;  
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;  
 KW gene; ds.

OS Homo sapiens.

PN WO200200928-A2.

PD 03-JAN-2002.

XX 02-JUL-2001; 2001WO-EP07537.

XX 30-JUN-2000; 2000DE-1032529.

PR 01-SEP-2000; 2000DE-1043826.

XX (EPiG-) EPIGENOMICS AG.

PA Olek A, Piepenbrock C, Berlin K;

PI WPI; 2002-130909/17.

XX Nucleic acid comprising fragment of chemically modified gene, useful  
 PT for diagnosis and treatment of diseases associated with abnormal  
 PT cytosine methylation -

PS Claim 1; SEQ ID NO 202; 32pp + Sequence Listing; German.

XX The present invention provides a number of human immune system associated  
 CC genes which are modified by the methylation of cytosines. The sequences  
 CC can be used in the diagnosis and treatment of immune system disorders,  
 CC including eye diseases such as retinopathy, neovascular glaucoma and  
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid  
 CC leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel  
 CC diseases. The present sequence is a gene of the invention.

XX Sequence 6049 BP; 1591 A; 109 C; 1429 G; 2920 T; 0 other;

Query Match 38.3%; Score 223; DB 24; Length 6049;  
 Best Local Similarity 70.4%; Pred. No. 7,8e-46;  
 Matches 298; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

QY 1 atggagacccagcagctggccacacagcggcgtctgtgacagctttagtatt 60  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1049 ATAGACACCCCAACCTGACCCCAACACACGAACTCTAATAACAACCTTTAATAATTAT 990  
 QY 61 aagctgagcagaggtatgtctgtgagctggcccgaggagggccagcagctgac 120  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 989 AAATCTAAACCAAAAATAATATATCTAATAAACCTGACCCGAAAAAACCACCAACTAAC 930  
 QY 121 ccgctgacacacagcagctgagcagctgagatgagctgagaccgcttcgagcagc 180  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 929 CCGCTACACCAACCACTACCACTAATAAATAAATTTGAAACCGGCTTCGACGACAC 870  
 QY 181 ttcctgattcggcggcgtcagctgacatgacacccagcagccacccagcagctcacc 240  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 869 TTCTCTAATCTAACGACTACACTACATNTAATACCCAACTCAACCCCAACGCTTACCC 810  
 QY 241 caggtctcgcagcagcttttcaagggggcccaactggggcgccgttgagccttctt 300  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 809 CAATCTCGATTAACCTTTTCAAAAAAACCCCAACCAACCCGCTTATTAACCTTCTT 750  
 QY 301 gttcttggcgtcagctgtgtgtcgtgagagtgtaacaaggagagatgacactgtgga 360  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 749 ATCTTTAAACTACACTATATTAATAAATAATCAACAAAAAATAAACCACCTAATAAAA 690











GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 6, 2002, 12:02:24 ; Search time 295.22 Seconds  
(without alignments)  
3384.744 Million cell updates/sec

Title: US-09-155-327E-8

Perfect score: 582  
1 atggcgacccacgcctcaac.....ccttttgcagcaagta 582

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

N.Geneseq-032802:\*

- 1: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*
- 2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*
- 3: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*
- 4: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*
- 5: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*
- 6: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:\*
- 7: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:\*
- 8: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:\*
- 9: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*
- 10: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:\*
- 11: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:\*
- 12: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:\*
- 13: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:\*
- 14: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:\*
- 15: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:\*
- 16: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:\*
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- 18: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:\*
- 19: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:\*
- 20: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:\*
- 21: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*
- 22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*
- 23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*
- 24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	577.8	99.3	581	20	AAV25133
2	563.4	96.8	581	18	AAV25133
3	563.4	96.8	581	20	AAV25133
4	558.2	95.9	579	19	AAV25133
5	558.2	95.9	579	20	AAV25133
6	520.2	89.4	581	20	AAV25133
7	519.6	89.3	583	18	AAV25133
8	519.6	89.3	583	20	AAV25133
9	515	88.3	579	19	AAV25133

10	515	88.5	579	20	AAV15946
11	372.8	64.1	1098	19	AAV41925
12	372.4	64.0	1864	19	AAV59630
13	218.6	37.6	6049	24	ABL32228
14	192.6	33.1	6049	24	ABL32228
15	148.4	25.5	150	22	ABV47382
16	148.4	25.5	150	22	ABA65269
17	148.4	25.5	150	22	ABA32370
18	148.4	25.5	150	22	ABA31683
19	148.4	25.5	150	22	AAK39424
20	148.4	25.5	150	22	AAI20236
21	148.4	25.5	150	22	AAI45438
22	148.4	25.5	150	22	AAI05940
23	135	23.2	1742	22	AAV75960
24	134.6	23.1	636	22	AAH48169
25	134.6	23.1	702	22	AAH43464
26	134.6	23.1	926	16	AAO81698
27	134.6	23.1	926	17	AAV40079
28	134.6	23.1	926	21	AAZ93614
29	134.6	23.1	926	21	AAI5189
30	134.6	23.1	926	22	AAZ90810
31	134.6	23.1	1236	22	AAV00247
32	134.6	23.1	7372	20	AAV33182
33	131.2	22.5	1455	22	AAV00250
34	129.6	22.3	747	22	AAV30926
35	126.8	21.8	600	22	ABA60917
36	126.8	21.8	600	22	ABA28894
37	126.8	21.8	600	22	AAK09207
38	126.8	21.8	600	22	AAK35096
39	126.8	21.8	600	22	AAI40812
40	126.8	21.8	720	22	AAH45295
41	125.8	21.6	555	22	AAV73433
42	125.8	21.6	555	22	ABA38761
43	125.8	21.6	555	22	AAK21876
44	125.8	21.6	555	22	AAK48039
45	125.8	21.6	555	22	AAI53868

#### ALIGNMENTS

RESULT 1  
AAV25133 standard; DNA: 581 BP.

AAV25133:

05-JUL-1999 (first entry)

Mouse bcl-w gene.

Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;  
animal model; ss.

Mus sp.

WO9913710-A1.

25-MAR-1999.

16-SEP-1998: 98WO-AU00764.

16-SEP-1997: 97AU-0009228.

(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

Adams J, Cory S, Gibson L, Koenigen F, Print C;  
WPL: 1999-243890/20.

P-PSDB: AAV05531.

An animal model exhibiting reduced levels of a Bcl-w protein and/or  
protein associated with Bcl-w

cdNA encoding the  
Nucleotide sequenc  
Human secreted pro  
Human immune syste  
Human breast cell  
Human foetal liver  
Probe #10836 for g  
Human brain expres  
Human bone marrow  
Probe #10169 for g  
Probe #14124 used  
Probe #5931 used t  
Rat wild-type Bcl-  
Mutant bcl-xl codi  
cdNA clone HP03564  
Human thymus Bcl-x  
Bcl-XL gene. Homo  
Bcl-x gene. Homo  
Human bcl-x cdna.  
Human Bcl-XL nucle  
Bcl-XL-DTR apoptos  
Base sequence of t  
Lfn-Bcl-XL apoptos  
Human Bcl-XL (tran  
Human foetal liver  
Probe #7360 for ge  
Human brain expres  
Human bone marrow  
Probe #9498 used t  
DNA encoding human  
Human foetal liver  
Probe #17227 for g  
Human brain expres  
Human bone marrow  
Probe #22554 used

XX Claim 3; Page 34; 52pp; English.  
 PS The present sequence is the mouse bcl-w gene encoding Bcl-w protein  
 CC (see AAY05531), a pro-survival member of the Bcl-2 family which is  
 CC widely expressed and which is essential for spermatogenesis. The  
 CC invention relates generally to a method of treatment and to an  
 CC animal model for the identification of molecules and genetic  
 CC sequences useful for inducing or reducing fertility of male  
 CC animals. Methods are provided for the treatment of infertility,  
 CC for reducing fertility, by modulating spermatogenesis. An animal  
 CC model carries a mutation in at least one allele of the human or  
 CC murine bcl-w gene or in a gene associated with bcl-w. Such animals  
 CC have disorganised seminiferous tubules and are substantially  
 CC infertile, but possess no other major abnormalities as determined  
 CC by histological examination. They can be used to screen for  
 CC therapeutic molecules including genetic sequences capable of  
 CC inducing, enhancing or otherwise facilitating spermatogenesis in  
 CC animals, or which can induce infertility.  
 XX  
 SO Sequence 581 BP; 106 A; 158 C; 200 G; 117 T; 0 other;

Query Match 99.3%; Score 577.8; DB 20; Length 581;  
 Best Local Similarity 99.7%; Pred. No. 3,4e-145;  
 Matches 579; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 atggagaccacccagctcaacccagacacagcgctcagtgctgagctatgagctat 60  
 DB 1 atggagaccacccagctcaacccagacacagcgctcagtgctgagctatgagctat 60  
 QY 61 agctcgaagcagaaggtatgtctgtgagctgagccttgaggagagccagccgac 120  
 DB 61 aagctgaagcagaaggtatgtctgtgagctgagccttgaggagagccagccgac 120  
 QY 121 ccgctgacacacagcagcagctgctgagcagagtttgagcccttcgcgcgac 180  
 DB 121 ccgctgacacacagcagcagctgctgagcagagtttgagcccttcgcgcgac 180  
 QY 181 ttcttgacctgctgcgctcagctacacagctgacccagcagcagcagcagcagc 240  
 DB 181 ttcttgacctgctgcgctcagctacacagctgacccagcagcagcagcagcagc 240  
 QY 241 caggtttccgagcagcagcttcccaaggggcccttaactgaggcgcttgtagctt 300  
 DB 241 caggtttccgagcagcagcttcccaaggggcccttaactgaggcgcttgtagctt 300  
 QY 301 gctcttgaggcgtccctgtgtgtgtagagtgtaacaagaatgaggccttgtagga 360  
 DB 301 gctcttgaggcgtccctgtgtgtgtagagtgtaacaagaatgaggccttgtagga 360  
 QY 361 caagtgcagagattgtagtggtcttaccctgagacagctctgctgagctatccacag 420  
 DB 361 caagtgcagagattgtagtggtcttaccctgagacagctctgctgagctatccacag 420  
 QY 421 agtggcgctgaggagaggtatgtctgtgagctgagccttgaggagagcagcag 480  
 DB 421 agtggcgctgaggagaggtatgtctgtgagctgagccttgaggagagcagcag 480  
 QY 481 cgtctgcgagaggaactggagcagctagtagagcagctgtagcagggcgctgagcag 540  
 DB 481 cgtctgcgagaggaactggagcagctagtagagcagctgtagcagggcgctgagcag 540  
 QY 541 ggggcctgtagaactgtagagcctttctgctagcaagtg 581  
 DB 541 ggggcctgtagaactgtagagcctttctgctagcaagtg 581

RESULT 2  
 AAT96578  
 ID AAT96578 standard; DNA: 581 BP.  
 XX  
 AC AAT96578;

XX 22-APR-1998 (first entry)  
 XX Mouse bcl-w DNA.  
 DE Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;  
 KW diagnosis; degenerative disease; ss.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..507  
 FT /\*tag= a  
 FT /product= bcl-w  
 FT /note= "q"  
 XX  
 PD W09735971-A1.  
 PD 02-OCT-1997.  
 PF 27-MAR-1997; 97MO-AU00199.  
 PF 27-MAR-1996; 96AU-0008965.  
 PR (AMRA-) AMRAD OPERATIONS PTY LTD.  
 PR Adams JM, Cory S, Gibson LM, Holmgreen SP;  
 DR WPL: 1997-489635/45.  
 DR P-PSDB; AAM36048.  
 XX  
 PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce  
 PT or inhibit cell survival, e.g. for treatment of cancer and  
 PT degenerative diseases  
 XX  
 PS Claim 3; Page 50-51; 86pp; English.  
 CC This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene  
 CC family. This gene promotes cell survival, so its modulation is useful in  
 CC treatment of cancer or auto-immune diseases, degenerative diseases (e.g.  
 CC stroke, Alzheimer's disease, myocardial infarct, muscular degeneration,  
 CC hypoxia, ischemia, human immunodeficiency virus infection or in cell  
 CC transplants. Up-regulation of the gene can also be used to modify cell  
 CC lines cultured in vivo, e.g. to develop new lines, to facilitate  
 CC isolation of hybridomas and to increase survival of primary explants  
 CC during genetic modification. It can be used to produce recombinant Bcl-w  
 CC for therapy, diagnosis, antibody production or screening of potential  
 CC modulators.  
 CC  
 SO Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 other;  
 Query Match 96.8%; Score 563.4; DB 18; Length 581;  
 Best Local Similarity 98.1%; Pred. No. 2.5e-141;  
 Matches 570; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
 QY 1 atggagaccacccagcctcaacccagacacacagcgctcagtgctgagctttagagctat 60  
 DB 1 atggagaccacccagcctcaacccagacacacagcgctcagtgctgagctttagagctat 60  
 QY 61 agctgagcagaagaggtatgtctgtgagctgagccttgaggagagccagccgac 120  
 DB 61 agctgagcagaagaggtatgtctgtgagctgagccttgaggagagccagccgac 120  
 QY 121 ccgctgacacacagcagcagctgctgagcagagtttgagaccctgttcgcgcgac 180  
 DB 121 ccgctgacacacagcagcagctgctgagcagagtttgagaccctgttcgcgcgac 180  
 QY 181 ttcttgacctgctgcgctcagctacacgtagacccagcagcagcagcagcagc 240  
 DB 181 ttcttgacctgctgcgctcagctacacgtagacccagcagcagcagcagcagc 240  
 QY 241 caggtttccgagcagcagcttcccaaggggcccttaactgaggcgcttgtagctt 300







## RESULT 7

AA96577 standard; DNA: 583 BP.

AC AAT96577;

DT 22-APR-1998 (first entry)

DE Human bcl-w DNA.

KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;  
diagnosis; degenerative disease; ss.

OS Homo sapiens.

FH Key Location/Qualifiers

FT 1..582  
FT /\*tag= a  
FT /product= bcl-w

PN W09735971-A1.

PD 02-OCT-1997.

PF 27-MAR-1997; 97MO-AU00199.

PR 27-MAR-1996; 96AU-0008965.

PA (AMRA-) AMRAD OPERATIONS PTY LTD.

PI Adams JM, Cory S, Gibson LM, Holmgreen SP;

DR WPI: 1997-489635/45.

DR P-PSDB; AAW36047.

PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce  
or inhibit cell survival, e.g. for treatment of cancer and  
degenerative diseases

PS Claim 3; Page 48; 86pp; English.

XX This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene  
XX family, extracted from an adult brain library. This gene promotes cell  
XX survival, so its modulation is useful in treatment of cancer or  
XX auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's  
XX disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia,  
XX human immunodeficiency virus infection or in cell transplants.  
XX Up-regulation of the gene can also be used to modify cell lines cultured  
XX in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas  
XX and to increase survival of primary explants during genetic modification.  
XX It can be used to produce recombinant Bcl-w for therapy, diagnosis,  
XX antibody production or screening of potential modulators.

Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other;

## Query Match

Best Local Similarity 89.3%; Score 519.6; DB 18; Length 583;

Matches 543; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1 atggcgagccagcctcaaccacagacacagcggtctagctgctgactttagatcat 60  
DB 1 atggcgagccagcctgcccagacacagcggtctgctgagactttagatcat 60  
QY 61 aggcctgagggagaggttatgtctgtgagctggtccctggggaagccagccagc 120  
DB 61 aagctcagggagagaggttatgtctgtgagctggtccctggggaagccagcagc 120  
QY 121 cgcgtgacacaaagcagctggtgagagctgttgaacccggttccgcgcagc 180  
DB 121 cgcgtgacacaaagcagctggtgagagctgttgaacccggttccgcgcagc 180  
QY 181 ttctcgacttgcgcgtcagctacagctgacccaggtcagccagcagcgttcacc 240

DB 181 ttctcgacttgcgcgtcagctacagctgacatgacccagccagccagcagcgttcacc 240  
QY 241 caggttccgagacactttccaaaggggcccttaactgtggccgtctgtgacatctt 300  
DB 241 caggttccgagacactttccaaaggggcccttaactgtggccgtctgtgacatctt 300  
QY 301 gtcttgggctgcccctgtgtctgagaggtcaacaagaatgtgagccttgttggga 360  
DB 301 ctcttgggctgcccctgtgtctgagaggtcaacaagaatgtgagccttgttggga 360  
QY 361 caatgacagatgtgagatgtgtgacctacccctgagacacgtctgtcgtacgtacacagc 420  
DB 361 caatgacagatgtgagatgtgtgacctacccctgagacacgtctgtcgtacgtacacagc 420  
QY 421 agtgcgctgctggcagagctacacagctcctacaggggagcggcccttggagagcgagc 480  
DB 421 agtgcgctgctggcagagctacacagctcctacaggggagcggcccttggagagcgagc 480  
QY 481 cgtctcgaggaggggaactgggcatcagtgagagacagtgctgacggggcgctgacactg 540  
DB 481 cgtctcgaggaggggaactgggcatcagtgagagacagtgctgacggggcgctgacactg 540  
QY 541 ggggcccctgtgaactgtagggccttttctgtacagatga 582  
DB 541 ggggcccctgtgaactgtagggccttttctgtacagatga 582

## RESULT 8

AA25134

ID AAX25134 standard; DNA: 583 BP.

AC AAX25134;

DT 05-JUL-1999 (first entry)

DE Human bcl-w gene derivative.

KW Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;  
animal model; ss.

OS Homo sapiens.

PN W09913710-A1.

PD 25-MAR-1999.

PF 16-SEP-1998; 98MO-AU00764.

PR 16-SEP-1997; 97AU-0009228.

PA (HALL-) HALL INST MEDICAL RES WALTER &amp; ELIZA.

PI Adams J, Cory S, Gibson L, Koentgen F, Print C;

DR WPI: 1999-243890/20.

DR P-PSDB; AAY05332.

PT An animal model exhibiting reduced levels of a Bcl-w protein and/or  
protein associated with Bcl-w

PS Disclosure; Page 36; 52pp; English.

XX The present sequence is described as a derivative of the human  
XX bcl-w gene (see AAX25132) and encodes Bcl-w protein (see AAY05332), a  
XX pro-survival member of the Bcl-2 family which is widely expressed  
XX and which is essential for spermatogenesis. The invention relates  
XX generally to a method of treatment and to an animal model for the  
XX identification of molecules and genetic sequences useful for  
XX inducing or reducing fertility of male animals. Methods are  
XX provided for the treatment of infertility, or for reducing  
XX fertility, by modulating spermatogenesis. An animal model carries  
XX a mutation is at least one allele of the human or murine bcl-w gene



or in a gene associated with bcl-2. Such animals have disorganised seminiferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility.

Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other;

Query Match 89.3%; Score 519.6; DB 20; Length 583;  
Best Local Similarity 93.3%; Pred. No. 1.3e-129;  
Matches 543; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

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61 agcgtgagcagagaggtatctgtgagctgctgagcgtgagagcgcgcgcgcac 120  
61 agcgtgagcagagaggtatctgtgagctgctgagcgtgagagcgcgcgcgcac 120  
121 ccgctgacacacagcagctgagcgtgagcgtgagcgtgagcgtgagcgtgagc 180  
121 ccgctgacacacagcagctgagcgtgagcgtgagcgtgagcgtgagcgtgagc 180  
181 tctctgacgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagc 240  
181 tctctgacgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagc 240  
241 caggttcacagcagcatttccacagcgtgagcgtgagcgtgagcgtgagcgtgagc 300  
241 caggttcacagcagcatttccacagcgtgagcgtgagcgtgagcgtgagcgtgagc 300  
301 gctcttgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagc 360  
301 gctcttgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagc 360  
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361 caagtgcaagagtgatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 420  
421 agtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480  
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481 cgtctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 540  
481 cgtctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 540  
541 ggggcccctgttaactgtagagcgttcttctgtagcaagtga 582  
541 ggggcccctgttaactgtagagcgttcttctgtagcaagtga 582

RESULT 9  
AAV28334  
ID AAV28334 standard; cDNA; 579 BP.  
XX AAV28334;  
XX 02-OCT-1998 (first entry)  
XX Human bcl-2 gene.  
XX ss; bcl-2; cell death pathway; apoptotic; apoptosis; human.  
XX Homo sapiens.  
XX Key 1.579 location/Qualifiers  
XX CDS /tag- a  
FT

/product= bcl-2  
/note= "No stop codon given"

US5789201-A.

04-AUG-1998.

11-FEB-1997; 97US-0798897.

23-FEB-1996; 96US-0012201.

11-FEB-1997; 97US-0798897.

(COCE-) COCENSYS INC.

Guastella J;

WPI; 1998-446079/38.

P-PSDB; AAM61392.

Claim 3; Column 15/16; 27pp; English.

The mammalian bcl-2 genes encode a protein that is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activity and the apoptosis blocking activity. bcl-2 falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell death is desired.

Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;

Query Match 88.5%; Score 515; DB 19; Length 579;  
Best Local Similarity 93.1%; Pred. No. 2.3e-128;  
Matches 539; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

1 atgagcaccacagctcaacccacacacagcgtctagctgacttgaagctat 60  
1 atgagcaccacagctcgcgcacacacacagcgtctgctgagcacttgaagctat 60  
61 agcgtgagcagagaggtatctgtgagctgctgagcgtgagagcgcgcgcgcac 120  
61 agcgtgagcagagaggtatctgtgagctgctgagcgtgagagcgcgcgcgcac 120  
121 ccgctgacacacagcagctgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagc 180  
121 ccgctgacacacagcagctgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagc 180  
181 tctctgacgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagc 240  
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301 gctcttgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagc 360  
301 gctcttgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagc 360  
361 caagtgcaagagtgatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 420  
361 caagtgcaagagtgatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 420  
421 agtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480  
421 agtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480  
421 agtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480

QY 481 cgtctgcggaggggaactgagcagtcagcaggggcccgtgacctg 540  
 Db 481 cgtctgcggaggggaactgagcagtcagcaggggcccgtgacctg 540  
 QY 541 ggggcccgtgtaactgtagggcctttttgtctagaag 579  
 Db 541 ggggcccgtgtaactgtagggcctttttgtctagaag 579

## RESULT 10

AAV415946 standard; CDNA; 579 BP.

AAV415946;

20-MAY-1999 (first entry)

CDNA encoding the human bcl-1-y protein.

Rat bcl-1-y protein; Rbcl-1-y: human bcl-1-y protein; Hbcl-1-y: bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite; ss.

Homo sapiens.

US5883229-A.

16-MAR-1999.

25-NOV-1997; 97US-0978523.

23-FEB-1996; 96US-0012201.

11-FEB-1997; 97US-0798897.

25-NOV-1997; 97US-0978523.

(COCE-) COCENSYS INC.

Guastella J;

WPI; 1999-214150/18.

P-PSDB; AAV97392.

Novel bcl-1-y homologues of the rat and human bcl-2 protein - useful for modulating programmed cell death

Disclosure: Columns 15-16; 26pp; English.

The present sequence encodes human bcl-1-y protein (Hbcl-1-y). The specification also describes rat bcl-1-y protein (Rbcl-1-y). Rbcl-1-y and Hbcl-1-y are homologues of the bcl-2 protein thought to be involved in programmed cell death (apoptosis and necrosis). Rbcl-1-y and Hbcl-1-y proteins may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, Alzheimer's Disease, neural and muscular degenerative diseases (especially multiple sclerosis), myocardial infarction, vitally induced cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis- conditions where cells under go premature cell death as a result of triggers which may or may not be apparent. They may also be used in this way to develop cell lines which remain viable in culture for an extended period. In contrast, if they act as cell death stimulators, Rbcl-1-y and Hbcl-1-y may be used to treat conditions associated with prolonged cell life span such as cancer (especially Kaposi's sarcoma and lung cancer) and autoimmune diseases. They may also be used to cause cell death in, and hence control, parasites.

Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;

Query Match 88.5%; Score 515; DB 20; Length 579;  
 Best Local Similarity 93.18; Pred. No. 2,3e-128;  
 Matches 539; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1 atggcagaccacagcttaaccacagacacagggcctagtgctgactgttaggcat 60  
 Db 1 atggcagaccacagcttaaccacagacacagggcctagtgctgactgttaggcat 60  
 QY 61 agcctgagcagagaggtatgtctgtgagctggtccttgggaaagccacagccgac 120  
 Db 61 aagctgagcagagaggtatgtctgtgagctggtccttgggaaagccacagccgac 120  
 QY 121 ccgctgacacacagcagctgagctgagcagagcttggagaccgcttccgcgac 180  
 Db 121 ccactgacacacagcagctgagctgagcagagcttggagaccgcttccgcgac 180  
 QY 181 ttcttgacctgacgctcagctacagctgagccagctcagccagcagcctcacc 240  
 Db 181 ttcttgacctgacgctcagctacagctgagccagctcagccagcagcctcacc 240  
 QY 241 caggttccgagcagactttccaaaggggccctacagctgagccgcttctgtgcatcctt 300  
 Db 241 caggttccgagcagactttccaaaggggccctacagctgagccgcttctgtgcatcctt 300  
 QY 301 gctcttgagcctgctcctgtgtgctgagagctgcaacaagaatggagccttgtgga 360  
 Db 301 gctcttgagcctgctcctgtgtgctgagagctgcaacaagaatggagccttgtgga 360  
 QY 361 caagtcagagatgtgctgctacacagctgagacagctgctgactgactcaccagc 420  
 Db 361 caagtcagagatgtgctgctacacagctgagacagctgctgactgactcaccagc 420  
 QY 421 agtgccgctgctgagcttaccagctcctacaggggagcggccttggagagcagcg 480  
 Db 421 agtgccgctgctgagcttaccagctcctacaggggagcggccttggagagcagcg 480  
 QY 481 cgtctgcggaggggaactggcagtcagtagagacagctgagcgggcccgtgacctg 540  
 Db 481 cgtctgcggaggggaactggcagtcagtagagacagctgagcgggcccgtgacctg 540  
 QY 541 ggggcccgtgtaactgtagggcctttttgtctagaag 579  
 Db 541 ggggcccgtgtaactgtagggcctttttgtctagaag 579

## RESULT 11

AAV41925 standard; CDNA; 1098 BP.

AAV41925;

20-NOV-1998 (first entry)

Nucleotide sequence of the CDNA clone Bcl-1-like (HAICH29).

Bcl-1-like (HAICH29): chronic inflammatory disease; allergic reaction; immunological disorder; autoimmune disease; anti-infectious agent; ss.

Homo sapiens.

Key Location/Qualifiers

CDS 1..1098 /tag= a /product= "Bcl-1-like (HAICH29) protein"

MO9831800-A2.

23-JUL-1998.

21-JAN-1998; 98WO-US00960.

21-JAN-1997; 97US-0034205.



CC This sequence represents a nucleic acid molecule designated Gene 120  
CC from the human cDNA clone HBBG264 (deposited as clone ATCC 97902 and  
CC ATCC 209048) which encodes a secreted human protein. The gene can be  
CC used to generate fusion proteins by linking to the gene to a human  
CC immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of  
CC the fused protein as compared to the human protein only.  
CC The invention relates to 186 novel genes and their fragments (nucleic  
CC acid sequences: AAV59511-V59812; amino acid sequences AAW47431-W5026)  
CC which are useful for preventing, treating or ameliorating medical  
CC conditions e.g. by protein or gene therapy. Also, pathological

QY	1	atggcgaccacccagagctcaaaccccaagaaacaacgagctctcagtcgactttgtagctat	60
Db	11	atggcgaccacccagagctcagccccagaaacaacgagctctcgtgtgcaagactttgtaggtat	70
QY	61	agagctgagacgaagaagggtctatgctcgtgtgagagctcgagccctcgaggaaagagccagccggac	120
Db	71	aagctgagagcagaagggtctatgctcgtgtgagagctcgagcccgagagagagccagcagctgac	130
QY	121	ccgctcgacacccaagccatgacgagctcgctctgagagacagttctgaaacccgtttctcgacgacc	180
Db	131	ccgctcgacacccaagacacgacgagctcgagctcagagctcgtgagatgagttcgcgaacccgttcgcgacac	190
QY	181	tctctctaacccctcgagccgtctcagctctcaacacgtgaccccaagctcagccccaagcaagcttcac	240
Db	191	tctctctaacccctcgagccgtctcagctctcaacacgtgaccccaagctcagccccaagcaagcttcac	250
QY	241	cagggtcttcgcgaagaaactttccaaagaggggcccctaaatctgggcccgtctctgtgacatctct	300
Db	251	cagggtcttcgcgaatgaacttttccaaagggggcccctaaatctgggcccgtctctgtgacatctct	310
QY	301	gtctcttgagagctccctctgctgtgctcgaagagttccaacaagaatgagagcccttctgtgtggga	360
Db	311	gtctcttgagagctccctctgctgtgctcgaagagttccaacaagaatgagagcccttctgtgtggga	370
QY	361	caaggtgcaagatctgagatggcgcctacacttgagagacaagcttcgtgctgactgagatcccaagc	420
Db	371	caaggtgcaagatctgagatggcgcctacacttgagagacaagcttcgtgctgactgagatcccaagc	430
QY	421	agtgctgagcgcctgg	432
Db	431	agtgctgagcgcctgg	442

PF 02-JUL-2001; 2001WO-EP07537  
XY



Sequence 150 BP; 25 A; 33 C; 65 G; 27 T; 0 other.

582

Search completed: June 6, 2002, 12:02:31  
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Query Match	Score	DB	Count	Len
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Thu Jun 6 16:39:24 2002

us-09-155-327e-8.rng

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